(FILE 'HCAPLUS' ENTERED AT 09:29:22 ON 04 DEC 2003) 673 SEA FILE=HCAPLUS ABB=ON PLU=ON COCCIDIOID? 242 SEA FILE=HCAPLUS ABB=ON PLU=ON L29 AND (PROTEIN OR L29 L30 POLYPEPTIDE OR PROTEIN OR PEPTIDE) L31 44 SEA FILE=HCAPLUS ABB=ON PLU=ON L30 AND VECTOR L32 14 SEA FILE=HCAPLUS ABB=ON PLU=ON L31 AND RECOMBIN? L32 ANSWER 1 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN ACCESSION NUMBER: 2003:846781 HCAPLUS TITLE: Cholera vaccine candidate 638: intranasal immunogenicity and expression of a foreign antigen from the pulmonary pathogen Coccidioides immitis AUTHOR(S): Silva, Anisia J.; Mohan, Archana; Benitez, Jorge CORPORATE SOURCE: Biochemistry and Immunology, Department of Microbiology, Morehouse School of Medicine, 720 Westview Dr., SW, Atlanta, GA, 30310-1495, USA Vaccine (2003), 21(32), 4715-4721 SOURCE: CODEN: VACCDE; ISSN: 0264-410X PUBLISHER: Elsevier Science Ltd. DOCUMENT TYPE: Journal LANGUAGE: English Vibrio cholerae strain 638 is a live genetically attenuated candidate cholera vaccine in which the CTXΦ prophage encoding cholera toxin has been deleted and hapA, encoding an extracellular Zn-dependent metalloprotease, was insertionally inactivated. Strain 638 was highly immunogenic when inoculated to adult Swiss mice by the intranasal route as judged by the induction of a strong serum vibriocidal antibody response. A side-by-side comparison of strain 638 with its isogenic hapA+ precursor (strain 81) in the above model indicated that inactivation of hapA does not affect immunogenicity. The spherule-associated antigen 2/proline-rich antigen (Ag2/PRA) of Coccidioides immitis has been shown to protect mice against coccidioidomycosis to an extent dependent on the modes of antigen presentation and challenge with C. immitis arthrospores. this work, we demonstrate the use of a live genetically attenuated V. cholerae strain to deliver Ag2/PRA. Ag2/PRA was expressed in 638 as a fusion protein with the Escherichia coli heat labile toxin B subunit leader peptide using the strong Tac promoter. The recombinant Ag2/PRA was efficiently expressed, processed and secreted to the periplasmic space. Intranasal immunizations of adult mice with strain 638 expressing Ag2/PRA induced serum vibriocidal antibody response to the vector strain and serum total IgG response to Ag2/PRA. Strain 638 expressing PRA could be recovered from trachea and lung up to 20 h after immunization but was effectively cleared 72 h post-inoculation. L32 ANSWER 2 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN 2003:454501 HCAPLUS ACCESSION NUMBER: 139:35072 DOCUMENT NUMBER: TITLE: Vectors comprising nucleotide

INVENTOR(S): McCreavy, David Thomas; Fraser, William Duncan; Gallagher, James Anthony

Searcher: Shears 308-4994

use as vaccines

sequences for target immunogen, PI31, CIIIA and antisense HERNA mRNA, and their uses including

PATENT ASSIGNEE(S): University of Liverpool, UK

SOURCE: PCT Int. Appl., 52 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

AB

PAT	ENT	NO.		KI	ND	DATE			Α	PPLI	CATI	ON NO	٥.	DATE		
· · · -	2003		-		_	2003			W	0 20	02-G	B551	2	2002	1206	
	W:	AE, CN, GE, LC, NO, TM,	AG, CO, GH, LK, NZ, TN,	AL, CR, GM, LR, OM, TR,	AM, CU, HR, LS, PH, TT,	AT, CZ, HU, LT, PL, TZ, MD,	AU, DE, ID, LU, PT, UA,	DK, IL, LV, RO, UG,	DM, IN, MA, RU, US,	DZ, IS, MD, SC,	EC, JP, MG, SD,	EE, KE, MK, SE,	ES, KG, MN, SG,	FI, KP, MW, SK,	GB, KR, MX, SL,	GD, KZ, MZ, TJ,
PRIORITY		GH, BG, MC, GQ,	GM, CH, NL, GW,	KE, CY, PT, ML,	LS, CZ, SE,	MW, DE, SI, NE,	MZ, DK, SK,	SD, EE, TR, TD,	SL, ES, BF, TG	FI, BJ, 001-	FR,	GB, CG,	GR, CI,	ΙE,	IT, GA, 1207	LU,

The invention provides vectors (such as viral vectors, plasmid vectors or phagemids) comprising: (a) a heterologous nucleotide sequence encoding an antigenic polypeptide from a pathogen (such as viral, bacterial, parasitic or fungal); (b) a nucleotide sequence encoding a protease inhibitor (such as human PI31); a nucleotide sequence for a constitutive, regulatable, and/or cell/tissue-specific promoter; and (d) a nucleotide sequence encoding an inhibitory RNA mols., specifically an antisense human HERNA oligonucleotides. The invention also provides vectors comprising a nucleotide sequence encoding CIITA, a polypeptide that stimulates the expression of MHC class II genes. The invention further provides the use of said vectors as vaccines in production of an immune response (humoral) to said antigens in an animal, such as human, wherein said vaccination may be against a viral, fungal, bacterial or parasitic disorder. Still further, the invention relates: (a) using said vectors in production of antibodies, wherein said antibodies may be of therapeutic and/or of diagnostic use; (b) that said vectors may be adapted for expression of humanized or chimeric antibodies; and (c) that said vectors may be used to used to immunize animals for production of hybridomas expressing a monoclonal antibody against antigen of interest. Finally, the invention provides the cDNA sequences of mouse CIITA, and human PI31, and partial cDNA sequence of human HERNA helicase. The invention related that the use of said vectors containing said sequences can be used to enhance secretion of translated immunogen, and enhance DNA vaccination bias away from an MHC class I event towards MHC class II event. In the examples, the invention presented the construction of two vectors, pcDNAFinal and pcDNA6TR-IRES-CIITA, wherein pcDNAFinal contains nucleotide sequences encoding immunogen parathyroid hormone-related protein (PTHrP), antisense HERNA mRNA, PI31 and CD4+ T-cell epitope from lymphocytic choriomeningitis virus and wherein

pcDNA6TR-IRES-CIITA encodes CIITA. Specifically, the invention related that: (a) antisense HERNA RNA can increase the transcriptional efficiency of **vectors** resulting in greater levels of transgene expression; (b) PI31 can inhibit proteasome digestion of **recombinant** antigen making it more assessable to MHC class II antigens; (c) inclusion of CD4+ T-cell epitope ensured that degraded immunogen-MHC class II complex bound to CD4+ T cells; and (d) inclusion of CIITA **protein** allowed for over-expression of MHC class II antigens.

L32 ANSWER 3 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:637813 HCAPLUS

DOCUMENT NUMBER: 137:180844

TITLE: Yeast Bax-responsive genes for drug target

identification in yeast and fungi

INVENTOR(S): Contreras, Roland Henri; Eberhardt, Ines;

Luyten, Walter Herman Maria Louis; Reekmans,

Rieka Josephina

PATENT ASSIGNEE(S): Janssen Pharmaceutica N.V., Belg.

SOURCE: PCT Int. Appl., 344 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

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PATENT NO.
                 KIND DATE
                                         APPLICATION NO. DATE
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                                          -----
    WO 2002064766 A2 20020822
WO 2002064766 A3 20030626
                           20020822
                                         WO 2001-EP15398 20011221
        W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
            CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
            GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
            LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
            NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
            TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG,
            KZ, MD, RU, TJ, TM
        RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
            CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
            SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
            SN, TD, TG
    EP 1346044
                     A2
                           20030924
                                          EP 2001-997983 20011221
            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
            PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.:
                                       EP 2000-870318
                                                       A 20001222
                                       EP 2001-870002
                                                      A 20010104
                                       EP 2001-870003
                                                      A 20010109
                                       WO 2001-EP15398 W 20011221
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AB The cDNAs for Saccharomyces cerevisiae genes responding to BAX gene expression as well as the **proteins** encoded by these cDNAs are disclosed. Addnl., Candida albicans and human homologs of the S. cerevisiae genes/**proteins** are provided. The invention describes the use of nucleic acids and **proteins** which are involved in apoptosis in yeast or fungi for the preparation of medicines for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compds. which selectively modulate the expression or functionality of said

proteins in the same or a parallel pathway. Also provided are compds. as well as pharmaceutical compns., medicines and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

L32 ANSWER 4 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2002:489694 HCAPLUS

DOCUMENT NUMBER:

137:92359

TITLE:

Role of signal sequence in vaccine-induced

protection against experimental

coccidioidomycosis

AUTHOR(S):

Jiang, Chengyong; Magee, D. Mitchell; Ivey, F.

Douglas; Cox, Rebecca A.

CORPORATE SOURCE:

Department of Microbiology, University of Texas

Health Science Center at San Antonio, San

Antonio, TX, 78229, USA

SOURCE:

Infection and Immunity (2002), 70(7), 3539-3545

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER:

American Society for Microbiology

DOCUMENT TYPE:

Journal

LANGUAGE: English The vaccine efficacy of the gene sequence encoding the signal peptide of the antigen known as antigen 2 or proline-rich antigen (Ag2/PRA), an immunodominant antigen present in the cell wall of the fungal pathogen Coccidioides immitis, was investigated in a murine model of coccidioidomycosis. Expression plasmids for Ag2/PRA(1-18) DNA (signal sequence), Ag2/PRA(19-194) DNA (lacking the signal sequence), and Aq2/PRA(1-194) DNA (full length) were inserted in the pVR1012 vector, and the constructs were used to vaccinate the highly susceptible BALB/c mouse strain. Immunization with the signal gene sequence significantly reduced the fungal burden in the lungs and spleens of mice 12 days after i.p. challenge with a LD of 2500 C.

immitis arthroconidia, to a level comparable to the protection induced in mice immunized with the full-length Ag2/PRA(1-194) DNA. The Aq2/PRA(19-194) gene protected mice but to a significantly lower level than the signal sequence or the full-length Ag2 gene. The immunizing capacity of Ag2/PRA(1-18) was not attributable to a nonspecific immunostimulatory effect of DNA, as evidenced by the fact that mice immunized with a frameshift mutation of Ag2/PRA(1-18) were not protected against challenge. Furthermore, a synthetic peptide corresponding to the translated sequence of

Aq2/PRA(1-18) DNA protected mice, albeit at a lower level than the Ag2/PRA(1-18) DNA vaccine. The protection induced with the signal gene vaccine correlated with the production of gamma interferon when splenocytes from Ag2/PRA(1-18)-immunized mice were stimulated with recombinant full-length Ag2 and was not associated with the

production of anti-Coccidioides IgG antibody. This is the first study to establish that a signal peptide sequence alone, administered as a gene vaccine or synthetic peptide

, can induce protective immunity against a microbial pathogen.

36

REFERENCE COUNT:

THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L32 ANSWER 5 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN 2002:366877 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 137:137416 Complementation of the ODC-Escherichia coli TITLE: (EWH319) null mutant by expression of the Coccidioides immitis ornithine decarboxylase (CiODC) gene AUTHOR(S): Guevara-Olvera, L.; Guevara-Gonzalez, R. G.; Munoz-Sanchez, C. I.; Gonzalez-Chavira, M. M. CORPORATE SOURCE: Inst. Tecnologico de Celaya, Depto. Ingenieria Bioquimica, Guanajuato, 38010, Mex. SOURCE: Informacion Tecnologica (2002), 13(2), 177-181 CODEN: ITECFG; ISSN: 0716-8756 Centro de Informacion Tecnologica PUBLISHER: DOCUMENT TYPE: Journal LANGUAGE: Spanish The aim of this study was to determine the function of the ornithine decarboxylase (CiODC) gene from Coccidioides immitis, a human respiratory fungal pathogen. A fragment of complementary DNA (cDNA) coding for CiODC protein was cloned into the pET-28b vector. The pET-CiODC recombinant plasmid was used to transform the EWH319 strain of Escherichia coli, which lacks the ODC gene and all others which synthesize polyamines and shows reduced growth due to this deficiency. Introduction of the transformant plasmid restored the bacterial growth in minimal M9 medium. The complemented strain EWH319.pET-CiODC showed ODC activity which was inhibited by 1,4-diamino-2-butanone (DAB) a competitive inhibitor which is specific for eukaryote ODCs. Based on the present results it was concluded that expression of the CiODC gene from Coccidioides immitis conferred a fundamental function for the growth of Escherichia coli. THERE ARE 20 CITED REFERENCES AVAILABLE REFERENCE COUNT: 20 FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT L32 ANSWER 6 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN 2002:107512 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 136:162279 Production of human monoclonal antibodies in TITLE: human B-lymphocyte hybridomas expressing an ectopic telomerase gene Dessain, Scott K.; Goldsby, Richard A. INVENTOR(S): PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA SOURCE: PCT Int. Appl., 74 pp. CODEN: PIXXD2 DOCUMENT TYPE: Patent LANGUAGE: English FAMILY ACC. NUM. COUNT: PATENT INFORMATION:

PATENT NO.	KIND DAT	re Al	PPLICATION NO.	DATE
WO 2002010352	A2 200	020207 W	2001-US24591	20010801
WO 2002010352	A3 200	030227		
W: AE, AG,	AL, AM, AT	T, AU, AZ, BA,	BB, BG, BR, BY	, BZ, CA, CH,
CN, CO,	CR, CU, CZ	Z, DE, DK, DM,	DZ, EC, EE, ES	, FI, GB, GD,
GE, GH,	GM, HR, HU	U, ID, IL, IN,	IS, JP, KE, KG	, KP, KR, KZ,
LC, LK,	LR, LS, LT	T, LU, LV, MA,	MD, MG, MK, MN	, MW, MX, MZ,

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10/081935
             NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,
             TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ,
            MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
            CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
             TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN,
            TD, TG
     US 2002045219
                            20020418
                                           US 2001-759984
                      A1
                                                            20010112
                                        US 2000-222473P P 20000802
PRIORITY APPLN. INFO.:
                                        US 2001-759984
                                                       A1 20010112
     The present invention relates to a method of making human monoclonal
     antibodies through the use of novel hybrid cells. In the invention,
     hybrid cells are created by combining three elements: a fusion
     partner cell, a fusion cell (in particular a human B-lymphocyte),
     and an ectopic telomerase gene. Mammalian cell lines that
     ectopically express telomerase and methods of using such cell lines
     in producing novel hybrid cells (hybridomas) that produce human
    monoclonal antibodies; human monoclonal antibodies produced by such
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novel hybridomas and DNA constructs useful for producing mammalian cell lines that ectopically express telomerase are described. The expression of an ectopic telomerase gene in hybrid cells formed from primary human B-lymphocytes and fusion partner cells (other human non-B lineage cells) improves their growth rate, level of Ig

expression, stability of Ig expression, and the ability to be cloned by limiting dilution A murine myeloma cell line that ectopically expressed human telomerase was created, as well as murine/human cell

L32 ANSWER 7 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

2001:935789 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 136:65197

TITLE: Sequences of antigenic polypeptides of

staphylococcus aureus and their uses in against

bacterial infection

Foster, Simon; McDowell, Philip; Brummell, INVENTOR(S):

Kirsty; Clarke, Simon

University of Sheffield, UK; Biosynexus Inc. PATENT ASSIGNEE(S):

SOURCE: PCT Int. Appl., 85 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent English LANGUAGE:

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

hybrids.

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PATENT NO.
                 KIND DATE
                                        APPLICATION NO.
                                        _____
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                 A1
                                      WO 2001-GB2685 20010620
WO 2001098499
                        20011227
       AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
        CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
        GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
        LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,
        TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ,
        MD, RU, TJ, TM
    RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
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        TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
        TG
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EP 1292681
                      Α1
                            20030319
                                           EP 2001-940746
                                                            20010620
            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
             PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
     BR 2001011823
                            20030610
                                           BR 2001-11823
                                                            20010620
                     Α
     NO 2002005838
                      Α
                            20030218
                                           NO 2002-5838
                                                            20021205
     US 2003186275
                            20031002
                                           US 2003-311879 20030318
                      A1
PRIORITY APPLN. INFO.:
                                        GB 2000-14907
                                                       A 20000620
                                        WO 2001-GB2685
                                                       W 20010620
AB
     The invention discloses methods for the identification of antigenic
     proteins expressed by pathogenic microbes, vaccines
     comprising the proteins, recombinant methods to
     manufacture the proteins and therapeutic antibodies directed to
     the proteins. In particular, the invention discloses
     amino acid sequences of staphylococcus aureus antigenic
    proteins, the DNA sequences encoding polypeptides
     and genomic DNA library of staphylococcus aureus. The invention
     also provides expression vectors encoding antigenic
    peptides, methods for the production of the proteins,
     antibodies to the proteins as well as methods of preparing
     the antibodies. The invention further provides vaccine comprising
     the antigenic proteins, pharmaceutical carrier, and
     adjuvant as well as methods of immunizing animals or humans.
REFERENCE COUNT:
                         2
                               THERE ARE 2 CITED REFERENCES AVAILABLE FOR
                               THIS RECORD. ALL CITATIONS AVAILABLE IN
                               THE RE FORMAT
L32 ANSWER 8 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
                        2001:309883 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         135:91197
                        Recombinant urease and urease DNA of
TITLE:
                         Coccidioides immitis elicit an
                         immunoprotective response against
                         coccidioidomycosis in mice
                         Li, Kun; Yu, Jieh-Juen; Hung, Chiung-Yu;
AUTHOR(S):
                         Lehmann, Paul F.; Cole, Garry T.
CORPORATE SOURCE:
                         Department of Microbiology and Immunology,
                         Medical College of Ohio, Toledo, OH, 43614-5806,
                         USA
SOURCE:
                         Infection and Immunity (2001), 69(5), 2878-2887
                        CODEN: INFIBR; ISSN: 0019-9567
                        American Society for Microbiology
PUBLISHER:
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         English
     Coccidioides immitis antigens which stimulate a T helper
     cell 1 (Th1) pathway of host immune response are considered to be
     essential components of a vaccine against coccidioidomycosis
       Recombinant urease (rURE) and recombinant
     heat shock protein 60 (rHSP60) of C. immitis were
     expressed in Escherichia coli and tested as vaccine candidates in
     BALB/c mice. A synthetic oligodeoxynucleotide which contained
     unmethylated CpG dinucleotides and was previously shown to enhance a
     murine Th1 response was used as an immunoadjuvant. T cells isolated
     from the spleens and lymph nodes of the rURE- and rHSP60-immune mice
     showed in vitro proliferative responses to the resp.
     recombinant protein, but only those T lymphocytes
     from rURE-immunized mice revealed markedly elevated levels of
     expression of selected Th1-type cytokine genes. BALB/c mice
     immunized s.c. with rURE and subsequently challenged by the i.p.
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route with a lethal inoculum of C. immitis arthroconidia demonstrated a significant reduction in the level of C. immitis infection compared to control animals. RHSP60 was much less effective as a protective antigen. Evaluation of cytokine gene expression in lung tissue and levels of recombinant urease-specific Igs (IgG1 vs. IgG2a) in murine sera at 12 days after challenge provided addnl. evidence that immunization with rURE stimulated a Th1 response to the pathogen. Urease was further evaluated by expression of the URE gene in a mammalian plasmid vector (pSecTag2A.URE) which was used to immunize mice by the intradermal route. In this case, 82% of the vector construct-immunized animals survived more than 40 days after i.p. infection, compared to only 10% of the mice immunized with the vector alone. In addition, 87% of the pSecTag2A.URE-immunized survivors had sterile lungs and spleens. These data support the need for further evaluation of the C. immitis urease as a candidate vaccine against coccidioidomycosis.

REFERENCE COUNT:

THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 9 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

44

ACCESSION NUMBER: 1999:83280 HCAPLUS

DOCUMENT NUMBER: 130:266091

TITLE: Genetic vaccination against Coccidioides

immitis: comparison of vaccine efficacy of recombinant antigen 2 and antigen 2 cDNA

AUTHOR(S): Jiang, Chengyong; Magee, D. Mitchell; Quitugua,

Teresa N.; Cox, Rebecca A.

CORPORATE SOURCE: Department of Clinical Investigation, Texas

Center for Infectious Disease, San Antonio, TX,

78223, USA

SOURCE: Infection and Immunity (1999), 67(2), 630-635

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

Previous studies from our laboratory established that C-ASWS, an alkali-soluble, water-soluble extract from cell walls of Coccidioides immitis, protects mice against lethal challenge with this fungus. The C-ASWS extract contains a glycosylated protein, designated antigen 2 (Ag2), and a polysaccharide antigen. We recently cloned Aq2 cDNA and showed that the recombinant fusion protein elicited strong delayed-type hypersensitivity responses in immunized mice. This investigation was undertaken to determine if the recombinant Ag2 protein, expressed as an Ag2-glutathione S-transferase (GST) fusion protein, or Ag2 cDNA would protect mice against lethal challenge with C. immitis. The recombinant Ag2-GST protein protected BALB/c mice against i.p. challenge with 250 arthroconidia, as assessed by a decrease in fungal CFU in tissues. The Ag2-GST-immunized mice did not show, however, an increased survival during a 30-day period postinfection. By contrast, immunization of mice with Ag2 cDNA ligated into the pVR1012 plasmid engendered protection against i.p. challenge with 2,500 arthroconidia and against pulmonary challenge with 50 arthroconidia. Vaccine efficacy paralleled the development of delayed-type hypersensitivity responses to C. immitis antiqen.

Whereas mice vaccinated with the **recombinant** Ag2-GST **protein** did not mount footpad hypersensitivity to C-ASWS or the **recombinant** Ag2-GST **protein**, mice vaccinated with the pVR1012-Ag2 construct mounted a strong footpad hypersensitivity and their spleen cells secreted gamma interferon upon in vitro stimulation with the Ag2-containing C-ASWS extract This is the first investigation to show that genetic immunization can protect against lethal challenge with C. immitis.

REFERENCE COUNT:

THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L32 ANSWER 10 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

50

ACCESSION NUMBER:

1999:18776 HCAPLUS

DOCUMENT NUMBER:

130:236203

TITLE:

Detecting serum antibodies to a purified recombinant proline-rich antigen of Coccidioides immitis in patients with

coccidioidomycosis

AUTHOR(S):

PUBLISHER:

Orsborn, Kris I.; Galgiani, John N.

CORPORATE SOURCE:

Research and Medical Services, Veterans Affairs Medical Center, University of Arizona, Tucson,

AZ, USA

SOURCE:

Clinical Infectious Diseases (1998), 27(6),

1475-1478

CODEN: CIDIEL; ISSN: 1058-4838 University of Chicago Press

DOCUMENT TYPE: LANGUAGE: Journal English

In previous work, antibodies in serum samples from patients with coccidioidomycosis were found to react with a proline-rich antigen (PRA) isolated from spherules of Coccidioides immitis, and the gene encoding this antigen was cloned. expressed and purified recombinant PRA (rPRA) by removing the majority of amino acids contributed by the vector from the fusion protein. Purified rPRA reacted with serum IgG antibodies in 37 of 42 patients with culture-proven progressive pulmonary or extrapulmonary coccidioidal disease; specific antibodies in dilns. ranging from 1:40 to 1:102,400 were demonstrated (sensitivity, 88%). In contrast, for >95% of patients without coccidioidomycosis reactivity of <1:40 was demonstrated (specificity, 97%). Of 18 patients with primary self-limited coccidioidomycosis, none had detectable antibodies in serum samples collected up to 141 days after illness began. The association of antibodies to rPRA with progressive infection

may have prognostic value. REFERENCE COUNT: 22

THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L32 ANSWER 11 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1996:391996 HCAPLUS

DOCUMENT NUMBER:

125:55750

TITLE:

Molecular cloning and characterization of

Coccidioides immitis antigen 2 cDNA

AUTHOR(S):

Zhu, Yufan; Yang, Chunmu; Magee, D. Mitchell;

Cox, Rebecca A.

CORPORATE SOURCE:

Dep. Clinical Investigation, Texas Center

Infectious Disease, San Antonio, TX, 78223, USA SOURCE: Infection and Immunity (1996), 64(7), 2695-2699

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

Previous expts. have provided evidence that Coccidioides immitis antigen 2 (Aq2) is a major T-cell-reactive component of mycelia and spherule cell walls. Here the authors report the identification and cloning of the cDNA that encodes Ag2 from a lambda ZAP cDNA expression library constructed from spherule-derived DNA sequence anal. established that the 1,255-bp clone contains a 174-bp 5' untranslated region, a 582-bp open reading frame which encodes for a protein consisting of 194 amino acids, and a 375-bp 3' untranslated region, including a poly(A) The recombinant Ag2 protein has a predicted mol. mass of 19.5 kDa and contains an 18-amino-acid N terminus which has been tentatively identified as a signal peptide. The Ag2 cDNA was ligated into the pGEX-4T-3 vector and expressed in Escherichia coli TG-1 cells as a glutathione S-transferase fusion protein. The recombinant fusion protein showed reactivity with sera from patients with coccidioidomycosis and elicited delayed-type footpad hypersensitivity responses in Coccidioides-immune mice. These results suggest that the Ag2 cDNA can be used for the large-scale production of this immunol. important protein.

L32 ANSWER 12 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:327965 HCAPLUS

DOCUMENT NUMBER: 125:28509

TITLE: Molecular cloning and characterization of the

Coccidioides immitis complement

fixation/chitinase antigen

AUTHOR(S): Yang, Chunmu; Zhu, Yufan; Magee, D. Mitchell;

Cox, Rebecca A.

Department Clinical Investigation, Texas Center Infectious disease, San Antonio, TX, 78223, USA

SOURCE: Infection and Immunity (1996), 64(6), 1992-1997

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

CORPORATE SOURCE:

AB Detection of anti-Coccidioides complement-fixing (CF) antibody is a valuable diagnostic and prognostic aid in coccidioidomycosis. The CF antibody response is directed against a heat-labile antigen that has chitinase activity, hereafter referred to as the CF/chitinase protein. To identify and clone this immunoreactive enzyme, the authors constructed a Coccidioides immitis cDNA lambda ZAP expression library from spherule RNA and detected fusion peptides expressing CF epitopes by immunoscreening. A cDNA clone consisting of 1623 bp was identified, sequenced, and found to contain a single open reading frame that encodes a protein of 47 kDa with 427 amino acids. Deduced amino acid sequence analyses showed that the cloned CF/chitinase cDNA contains a 35-amino-acid region, beginning at Ser-18 and ending at Arg-52, which has 92% homol. with the reported N-terminal amino acid sequence of authentic CF/chitinase

protein. The first 17 amino acids in the deduced sequence
of the cloned cDNA are not present on the mature CF/chitinase
protein, suggesting that it may be a signal peptide
. Expression of the CF/chitinase cDNA insert by using the pGEX-4T-3
vector yields a fusion peptide that bears
CF-specific epitopes and shows chitinase activity. The CF/chitinase
clone will enable large-scale production of the recombinant CF
antigen for use in immunoassays and facilitate studies on the role
of chitinase in the morphogenesis of C immitis.

L32 ANSWER 13 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:832234 HCAPLUS

DOCUMENT NUMBER: 124:2086

TITLE: Molecular and biochemical characterization of a

Coccidioides immitis-specific antigen

AUTHOR(S): Pan, Shuchong; Cole, Garry T.

CORPORATE SOURCE: Department of Microbiology, Medical College of

Ohio, Toledo, OH, 43699-008, USA

SOURCE: Infection and Immunity (1995), 63(10), 3994-4002

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

Results of earlier investigations have indicated that the saprobic phase of Coccidioides immitis produces a heat-stable, 19-kDa antigen with serine proteinase activity which has been suggested to be specific for this pathogenic fungus. In the present study the authors have determined the N-terminal and partial internal amino acid sequences of the purified, 19-kDa antigen, cloned the gene which encodes this polypeptide, and confirmed that the secreted proteinase is a Coccidioides-specific antigen (CS-Aq). Both the genomic and cDNA sequences are reported and reveal that the csa gene which encodes this antigen has no introns. A 543-bp open reading frame encodes a 181-amino-acid-containing protein with a predicted mols. mass of 19.8 kDa and an isoelec. point of 8.3. The csa gene was localized on chromosome I of three representative C. immitis clin. isolates on the basis of Southern hybridizations. Expression of the csa gene in Escherichia coli using the pET21a plasmid vector yielded a recombinant protein that was recognized in immunoblot assays by antibody raised to the purified 19-kDa CS-Aq. Secretion of the native antigen is suggested to occur by cleavage of a putative 23-residue signal peptide. The native CS-Ag showed a low degree of glycosylation. Anal. of the carbohydrate composition of the CS-Ag revealed xylose, mannose, galactose, and qlucose. However, the purified antigen showed no affinity for Con A. A PCR method with specificity and high sensitivity for detection of C. immitis genomic DNA, using a pair of synthetic oligonucleotide primers whose sequences were based on that of the csa gene, was developed. A 520-bp product was amplified only when C. immitis genomic DNA was used as the template. The lower limits of DNA detection using this PCR method were 1 pg of C. immitis genomic DNA by ethidium bromide staining and 100 fg after Southern hybridization. The csa gene-based PCR method for detection of C. immitis DNA is useful for culture identification and may have clin. applications for the diagnosis of coccidioidal infections.

L32 ANSWER 14 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:267638 HCAPLUS

DOCUMENT NUMBER: 120:267638

TITLE: Identification of antigens of

Coccidioides immitis which stimulated

immune T lymphocytes

AUTHOR(S): Cole, Garry T.; Kirkland, Theo N.

CORPORATE SOURCE: Dep. Bot., Univ. Texas, Austin, TX, 78713, USA

SOURCE: Archives of Medical Research (1993), 24(3),

281-91

CODEN: AEDEER; ISSN: 0188-4409

DOCUMENT TYPE: Journal LANGUAGE: English

T-cell mediated immune response to coccidioidomycosis has been shown to be the principal mechanism of resistance to this respiratory fungal disease in exptl. animals. In this study, a Coccidioides immitis antigen-specific murine T-cell line was used to identify macromols. capable of eliciting an immune mouse T-cell proliferative response. The murine T-cell line was selected on the basis of its strong pos. response to a soluble conidial wall fraction (SCWF), which had previously been shown to be reactive in humoral and cellular immunoassays. An antigen-specific T-cell line rather than T-cell clones was used to identify multiple antigens. The T-cell immunoblot method was employed first to identify immunoreactive subfractions of the SCWF, and then to identify T-cell fusion proteins (FPs) obtained from a cDNA expression library constructed in Agtll. The library was screened with anti-SCWF. The nucleotide sequence of a 0.2-kb cDNA insert encoding a FP which elicited vigorous T-cell response was determined A construct of this insert was subcloned into the pET expression vector system and 6.5-kDa recombinant protein (RP) expressed in Escherichia coli was isolated. The RP and FP were shown to be homologous on the basis of identify of their amino acid sequences. Antibody raised in guinea pigs against the RP recognized a 59-kDa native protein of the mycelial culture filtrate produced by 3 sep. strains of C. immitis, and reacted with the cell wall of arthroconidia as detected by immunofluorescence microscopy. In this study, a potentially important T-cell stimulating antigen of C. immitis was identified and partly characterized.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 09:34:38 ON 04 DEC 2003)

L33 37 S L32

L34 18 DUP REM L33 (19 DUPLICATES REMOVED)

L34 ANSWER 1 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-829776 [77] WPIDS

CROSS REFERENCE: 1999-551417 [46]; 2002-606631 [65]

DOC. NO. NON-CPI: N2003-662909 DOC. NO. CPI: C2003-233753

TITLE: Novel chitin-binding, chitinase-inactive polypeptide comprising a chitin-binding

fragment, useful for treating fungal infections.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): GRAY, P W; TJOELKER, L W

PATENT ASSIGNEE(S): (GRAY-I) GRAY P W; (TJOE-I) TJOELKER L W

COUNTRY COUNT: 1

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG US 2003143216 A1 20030731 (200377) * 33

APPLICATION DETAILS:

PATENT NO KIND	 APPLICATION	DATE
US 2003143216 A1	 US 1998-39198 US 1999-267574	19980312 19990312
	US 2002-161547	20020603

FILING DETAILS:

PATENT NO) KIND		PATEN'	r no
US 200314		 CIP of Div ex	US 620 US 639	

PRIORITY APPLN. INFO: US 1999-267574 19990312; US 1998-39198 19980312; US 2002-161547 20020603

2003-829776 [77] WPIDS ΑN

1999-551417 [46]; 2002-606631 [65] CR

AΒ US2003143216 A UPAB: 20031128

> NOVELTY - A chitin-binding, chitinase-inactive polypeptide (I) comprising a chitin-binding fragment of 54 C-terminal amino acids of a fully defined human chitinase sequence (S1) of 466 amino acids as given in the specification, is new. (I) is chosen from polypeptides having sequence of amino acid residues 347-397 to 445 of (S1).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

- (1) a fusion protein (II) comprising (I) fused to a heterologous polypeptide;
 - (2) a composition (III) comprising (I) and a diluent;
- (3) a composition (IV) comprising (I) conjugated to an antifungal agent;
- (4) a composition (V) comprising (I) conjugated to a detectable label;
- (5) a kit (VI) for diagnosing the presence of chitin in a sample comprising the composition;
 - (6) a purified, isolated polynucleotide (VII) encoding (I);
 - (7) a vector (VIII) comprising (VII);
- (8) a host cell (IX) transformed or transfected with (VII) in a manner allowing the expression of (I) encoded by (VII) in (IX);
- (9) a **polypeptide** produced by culturing (IX); and (10) a monoclonal antibody (X) that specifically binds to an epitope within the 54C-terminal amino acid of (S1). ACTIVITY - Fungicide.

Anti-fungal activity of recombinant chitinase in vivo in mice was determined as follows. Female Balb/c mice, 6-8 weeks old, were administered 0.5, 5.0, 50 mg/kg recombinant human chitinase by intravenous injection in the tail vein. The mice was infected with the fungi, varying doses of test drug was administered to the animals and their survival is measured over time. Specifically, acute systemic candidiasis was achieved in mice by intraperitoneal or intravenous challenge of 10 multiply 106 colony forming units (CFU) candida albicans. The recombinant

chitinase was administered before or at 1 to 5 hours after challenge, and the number of survivors was determined after five days. In addition, the mice can be sacrificed and fungal load can be determined in specific organs. Alternatively, the mice were challenged with lower doses of fungi, e.g., Aspergillus (8-10 multiply 106 CFU) or Candida (1 multiply 106 CFU) in which case survival can be measured at more distant time points, e.g. 45 days. The long term fungicidal/fungistatic activity of a chitinase may be evaluated by continuing therapy for a week or more, e.g. 11 days, and following the animals over several weeks, e.g. 18 days to one month. The result showed that effective anti-fungal agent (recombinant chitinase) enhanced the long term survival of animals and reduced fungal load in blood and organs.

MECHANISM OF ACTION - Lysis of fungal cell wall and membrane. USE - (III) or (IV) is useful for treating (M1) fungal infection which involves administering (III) or (IV) to a subject suffering from fungal infection. (M1) further comprises administering a non-chitinase antifungal agent. (V) is useful for detecting the presence of chitin in a sample which involves contacting the sample with (V) and determining the amount of labeled polypeptide bound to chitin. (claimed).

(III), (IV) or (V) is useful for treating fungal infections such as candidiasis, aspergillosis, coccidioidomycosis, blastomycosis, paracoccidioidomycosis, histoplasmosis, cryptococcosis, chromoblastomycosis, sporotrichosis, mucormycosis, and the dermatophytoses can manifest as acute or chronic disease. (VII) is useful in hybridization assays to detect the capacity of cells to synthesize chitinase and for diagnostic methods useful for identifying a genetic alteration(s) in the chitinase locus that underlies a disease state or states. (X) is useful for detecting or quantifying the presence of chitin-binding domain, and for detecting or quantifying the presence of yeast or fungi, e.g., by adding a chitin-binding domain which binds to the yeast of fungi. (X) is also useful for detecting chitin-binding domain in human blood samples which indicates a disease state involving chitinase, such as Gaucher's disease. Dwg.0/0

L34 ANSWER 2 OF 18 MEDLINE on STN DUPLICATE 1

2003510266 IN-PROCESS ACCESSION NUMBER:

DOCUMENT NUMBER: 22949199 PubMed ID: 14585681

TITLE: Cholera vaccine candidate 638: intranasal

immunogenicity and expression of a foreign antigen

from the pulmonary pathogen Coccidioides

immitis.

Silva Anisia J; Mohan Archana; Benitez Jorge A AUTHOR: CORPORATE SOURCE: Department of Microbiology, Biochemistry and

Immunology, Morehouse School of Medicine, 720 Westview Dr., SW 30310-1495, Atlanta, GA, USA.

VACCINE, (2003 Dec 1) 21 (32) 4715-21.

Journal code: 8406899. ISSN: 0264-410X.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

SOURCE:

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20031031

Last Updated on STN: 20031031

AB Vibrio cholerae strain 638 is a live genetically attenuated

candidate cholera vaccine in which the CTXPhi prophage encoding cholera toxin has been deleted and hapA, encoding an extracellular Zn-dependent metalloprotease, was insertionally inactivated. Strain 638 was highly immunogenic when inoculated to adult Swiss mice by the intranasal route as judged by the induction of a strong serum vibriocidal antibody response. A side-by-side comparison of strain 638 with its isogenic hapA(+) precursor (strain 81) in the above model indicated that inactivation of hapA does not affect immunogenicity. The spherule-associated antigen 2/proline-rich antigen (Ag2/PRA) of Coccidioides immitis has been shown to protect mice against coccidioidomycosis to an extent dependent on the modes of antigen presentation and challenge with C. immitis arthrospores. In this work, we demonstrate the use of a live genetically attenuated V. cholerae strain to deliver Ag2/PRA. Ag2/PRA was expressed in 638 as a fusion protein with the Escherichia coli heat labile toxin B subunit leader peptide using the strong Tac promoter. The recombinant Ag2/PRA was efficiently expressed, processed and secreted to the periplasmic space. Intranasal immunizations of adult mice with strain 638 expressing Ag2/PRA induced serum vibriocidal antibody response to the vector strain and serum total IgG response to Ag2/PRA. Strain 638 expressing PRA could be recovered from trachea and lung up to 20h after immunization but was effectively cleared 72h post-inoculation.

L34 ANSWER 3 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-120579 [11] WPIDS DOC. NO. NON-CPI: N2003-096057

DOC. NO. NON-CPI: N2003-096057 DOC. NO. CPI: C2003-031163

TITLE: Identifying biologically active agents comprises cloning transfected cells into a cell array,

exposing the array to an agent to be tested, and detecting signals generated by a reporter molecule

as a result of exposure to the agent.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): ANDREWS, P; DRAPER, J; WALSH, J

PATENT ASSIGNEE(S): (AXOR-N) AXORDIA LTD

COUNTRY COUNT: 100

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2002090992 A2 20021114 (200311)* EN 90

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP

KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ

NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ

UA UG US UZ VN YU ZA ZM ZW

APPLICATION DETAILS:

PRIORITY APPLN. INFO: GB 2001-11004 20010504

AN 2003-120579 [11] WPIDS

AB WO 200290992 A UPAB: 20030214

NOVELTY - Screening (M1) for identifying biologically active agents, comprises:

- (i) providing a population of cells stably transfected with a nucleic acid encoding a reporter molecule;
 - (ii) cloning the transfected cells into a cell array;
- (iii) exposing the array to at least one agent to be tested; and
- (iv) detecting a signal generated by the reporter molecule as a result of exposure to the agent.

DETAILED DESCRIPTION - Screening (M1) for identifying biologically active agents, comprises:

- (i) providing a population of cells which have been stably transfected with a nucleic acid molecule encoding a reporter molecule;
 - (ii) cloning the transfected cells into a cell array;
- (iii) exposing the array to at least one agent to be tested; and
- (iv) detecting a signal generated by the reporter molecule as a result of exposure to the agent.

INDEPENDENT CLAIMS are also included for the following:

- (1) An agent identified by M1;
- (2) A cell or a cell array obtained by M1;
- (3) Screening (M2) for the isolation of a gene, comprising:
- (a) steps (i)-(iv) of M1;
- (b) extracting nucleic acid from a cell sample comprising the cell array; and
- (c) determining the sequence of at least part of the genomic region into which the nucleic acid encoding the reporter molecule has integrated;
- (4) Comparing the biological activity of a reference agent with at least one other agent, comprising:
 - (a) steps (i) and (ii) of the above method;
 - (b) preparing a duplicate array;
 - (c) step (iii) of the above method;
 - (d) exposing the duplicate array to a reference agent; and
- (e) detecting a signal generated by the reporter molecule as a result of exposure to the agent and to the reference agent; and
- (5) A **vector** comprising a reporter molecule, a splice acceptor site and an internal ribosome entry site, where the splice acceptor and the internal ribosome entry site are operably linked to facilitate expression of the reporter molecule.
- USE The method is useful in identifying biologically active agents and the genes through which the agents act, in screening potential drugs for their ability to activate certain drug targets in a high-throughput assay, in identifying relationships between signaling pathways and specific signals that could be useful in eventually directing the differentiation of embryonic stem cells, and in toxicology assays by testing for unwanted activation or inhibition of specific signaling pathways. The **vector** is useful in carrying out the above methods (claimed). Dwg.0/99

L34 ANSWER 4 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-566694 [60] WPIDS

DOC. NO. CPI: C2002-160652

TITLE: Constructing strains for identifying gene products

as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene

and placing other allele of the gene under

conditional expression.

DERWENT CLASS: B04 C06 D16

INVENTOR(S): BOONE, C; BUSSEY, H; JIANG, B; OHLSEN, K L; ROEMER,

Т

PATENT ASSIGNEE(S): (ELIT-N) ELITRA PHARM INC

COUNTRY COUNT: 101

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2002053728 A2 20020711 (200260)* EN 167

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ

NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ

UA UG US UZ VN YU ZA ZW

US 2003180953 A1 20030925 (200364)

EP 1348027 A2 20031001 (200365) EN

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

APPLICATION DETAILS:

PAT	TENT NO F	CIND		API	PLICATION	DATE
WO	2002053728	A2		WO	2001-US49486	20011226
US	2003180953	A1	Provisional	US	2000-259128P	20001229
			CIP of	US	2001-792024	20010220
			Provisional	US	2001-314050P	20010822
				US	2001-32585	20011220
ΕP	1348027	A2		EP	2001-991419	20011226
				WO	2001-US49486	20011226

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1348027	A2 Based on	WO 2002053728

PRIORITY APPLN. INFO: US 2001-314050P 20010822; US 2000-259128P

20001229; US 2001-792024 20010220; US

2001-32585 20011220

AN 2002-566694 [60] WPIDS

AB WO 200253728 A UPAB: 20020919

NOVELTY - Constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker, and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter, si new.

DETAILED DESCRIPTION - Constructing (M1) a strain of diploid

fungal cells in which both alleles of a gene are modified, comprising constructing a strain of diploid fungal cells in which both alleles of a gene are modified, comprises modifying one allele in diploid fungal cells by recombination using a gene disruption cassette comprising a first nucleotide sequence encoding an expressible selectable marker, to provide heterozygous diploid fungal cells in which the first allele is inactivated, and modifying the second allele by recombination using a promoter replacement fragment comprising a second nucleotide sequence encoding a heterologous promoter, so that expression of the second allele is regulated by the heterologous promoter, where the gene encodes a polypeptide required for proliferation of Candida albicans, where the **polypeptide** is chosen from the amino acid sequence (S1) of 932 essential genes listed in the specification. INDEPENDENT CLAIMS are also included for the following:

- (1) assembling (M2) a collection of diploid fungal cells each compring modified alleles of a different gene, by modifying both alleles of the gene by (M1) and repeating the steps several times, where a different gene is modified with each repetition;
- (2) a strain (I) of diploid fungal cells comprising modified alleles of a gene, where the first allele is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker, and the expression of the second allele is regulated by a heterologous promoter that is operably linked to the coding region of the second allele;
 - (3) a collection of diploid fungal strains comprising (I);
- (4) a nucleic acid molecule microarray comprising several nucleic acid molecules, each comprising a nucleotide sequence that is hybridizable to a target nucleotide sequence chosen from 932 nucleotide sequences (S2) of the open reading frame (ORF) of essential genes, gene names listed in the specification, no sequences are given;
- (5) a purified or isolated nucleic acid molecule (II) comprising a nucleotide sequence encoding a gene product required for proliferation of C. albicans, and comprising (S1);
- (6) a nucleic acid molecule (III) comprising at least 10-100 consecutive nucleotides of (S2);
- (7) a purified or isolated nucleic acid molecule (IV) obtained from an organism other than C. albicans or Saccharomyces cerevisiae comprising at least 30 % identity to a (S2), as determined using BLASTN version 2.0 with the default parameters;
- (8) a vector containing the promoter operably linked to (II), (III) or (IV);
 (9) a host cell containing the **vector** of (9);
- (10) a purified or isolated polypeptide comprising a sequence chosen from 61 sequences not given in the specification;
- (11) a purified or isolated polypeptide (V) obtained from an organism other than C. albicans or S. cerevisiae comprising at least 30 % similarity to (S1), as determined using FASTA version 3.0t78 with the default parameters;
- (12) a fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, the fragment at least 6 consecutive residues of (S1);
 - (13) producing (V);
- (14) identifying (M3) a compound which modulates the activity of a gene product encoded by a nucleic acid comprising (S2), by contacting the gene product with a compound, and determining if the

compound modulates the activity of the gene product;

- (15) eliciting an immune response in an animal, by introducing into the animal a composition comprising an isolated **polypeptide** having 6 consecutive residues of (S1);
- (16) a strain of C. albicans where a first allele of a gene comprising (S2) is inactive and a second allele is under the control of a heterologous promoter;
- (17) identifying a compound or binding partner that binds to a **polypeptide** comprising (S1) or its fragment;
- (18) identifying (M4) a compound having the ability to inhibit growth or proliferation of C. albicans, by reducing the level or activity of a gene product encoded by (S2) in the C. albicans cell relative to a wild type cell, where the reduced level is not lethal to the cell, contacting the cell with a compound and determining if the compound inhibits the growth or proliferation of the cell;
- (19) inhibiting (M5) growth or proliferation of C. albicans cells, by contacting the cells with the compound that reduce the level of or inhibit the activity of (S1) or (S2);
- (20) manufacturing an antimycotic compound, by screening several compounds to identify a compound that reduces the activity or level of a gene product encoded by (S2) and manufacturing the compound identified;
- (21) treating (M6) an infection of a subject by C. albicans, by administering compound (C) that reduces the activity or level of a gene product encoded by (S2);
 - (22) an antibody preparation (VI) which binds (V); and
- (23) correlating changes in the levels of **proteins** or gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell, by generating a first **protein** expression profile for or transcription profile for a control diploid fungal cell which comprises two wild type alleles of the gene, culturing (I) under conditions where the second allele of the gene is underexpressed, not expressed or overexpressed, and generating a second **protein** expression profile for the cultured cells, and comparing the profiles.

ACTIVITY - Fungicide; Plant Antifungal.

No biological data is given.

MECHANISM OF ACTION - None given.

USE - (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M3) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. (M4) is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans. (M5) is useful for inhibiting growth or proliferation of C. albicans cells. (M6) is useful for treating infection by C. albicans. (All claimed). Dwg.0/6

L34 ANSWER 5 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-666824 [71] WPIDS

DOC. NO. CPI: C2002-187137

TITLE: Nucleic acid molecules comprising fungal, e.g.

Cochliobolus heterostrophus, genes from a **peptide** synthetase gene cluster, useful for

identifying anti-fungal agents for treating fungal

infections such as pneumonia and arthritis.

DERWENT CLASS: C07 D16

INVENTOR(S): LU, S; TURGEON, B G; YODER, O

PATENT ASSIGNEE(S): (CORR) CORNELL RES FOUND INC; (LUSS-I) LU S; (SYGN)

SYNGENTA PARTICIPATIONS AG; (TURG-I) TURGEON B G;

(YODE-I) YODER O

COUNTRY COUNT: 100

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2002042444 A2 20020530 (200271)* EN 316

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP

KE KG KP KR KZ LC LK LR \cdot LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA

UG US UZ VN YU ZA ZM ZW

AU 2002036448 A 20020603 (200277)

APPLICATION DETAILS:

PATENT NO KI	ND APP	PLICATION	DATE
WO 2002042444 A	A2 WO	2001-US43381	20011121
AU 2002036448 A	A AU	2002-36448	20011121

FILING DETAILS:

PRIORITY APPLN. INFO: US 2000-252732P 20001122; US 2000-252649P

20001122

AN 2002-666824 [71] WPIDS

AB WO 200242444 A UPAB: 20030410

NOVELTY - Nucleic acid molecules comprising fungal, e.g.

Cochliobolus heterostrophus, genes from a peptide

synthetase gene cluster, e.g. an iron reductase and/or a permease or a major facilitator superfamily (MFS) transporter, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for

nucleic acid sequence (NA1) comprising an open reading frame comprising the 2435 (S46), 1836 (S48), or 2073 (S55) base pair (bp) sequence defined in the specification, or their complements;

(2) an isolated polynucleotide (N2) comprising a fungal nucleic

acid segment which is substantially similar to NA1, or its complements;

- (3) an isolated polynucleotide (N3) comprising a fungal nucleic acid segment which hybridizes under stringent hybridization conditions to S46, S48, S55, or its complements;
- (4) an isolated polypeptide (P1) encoded by N1, N2 or N3;
- (5) an expression cassette comprising a promoter operably linked to N1, N2 or N3;
- (6) a **recombinant vector** comprising N1, N2 or N3, where the **vector** is capable of being stably transformed into a host cell;
- (7) a host cell comprising the expression cassette of (5) or the **vector** of (6);
- (8) a method (M1) for identifying an agent having fungicidal or mycocidal activity, comprising contacting a fungus with an agent that binds to or inhibits P1, and identifying an agent having fungicidal or mycocidal activity;
- (9) a method (M2) for identifying an inhibitor of a **polypeptide**, comprising contacting a host cell which expresses a **polypeptide** encoded by N1, N2 or N3 with an agent, and identifying an agent that inhibits the activity of the **polypeptide**;
 - (10) an agent identified by the M1 or M2;
- (11) a method of inhibiting the growth or pathogenicity of a fungus, comprising contacting the fungus with the agent of (10) in an amount sufficient to inhibit the growth or pathogenicity of the fungus;
- (12) a method for identifying an agent that modulates a polypeptide associated with pathogenicity of a fungus, comprising contacting a fungus with an agent that binds P1, and identifying an agent that modulates the pathogenicity of the fungus;
- (13) a method for identifying an agent that modulates the pathogenicity of a fungus, comprising contacting a fungus with an agent that inhibits the activity of Pl, and identifying an agent that modulates the pathogenicity of the fungus;
- (14) a method (M3) of identifying agents that alter the phenotype of a fungal pathogen or mycogen, comprising:
- (a) contacting an agent to be tested with one or more cells of a fungal pathogen or mycogen where:
- (i) the cells comprise a nucleotide sequence encoding a **polypeptide** that is substantially similar to the 812 (S47), 611 (S49) or 487 (S56) amino acid sequence defined in the specification; or
- (ii) the cells have a mutation in N1, N2 or N3, where the mutation results in overexpression or underexpression of the encoded polypeptide; and
- (b) detecting or determining whether the agent selectively modulates expression or function or metabolic pathways associated with the **polypeptide**, therefore altering a phenotype of the cells relative to cells not contacted with the agent;
 - (15) an isolated antibody (Abl) which specifically binds to P1;
- (16) a method (M4) to prevent or inhibit infection of an animal or plant by a fungal pathogen, comprising administering to the animal or plant an effective amount of the agent of (10) for a time and under conditions sufficient to inhibit or prevent fungal growth or reproduction;
 - (17) the sequence of N1, N2 or N3, or the amino acid sequence

of Pl stored on a computer readable medium; and

(18) a transformed plant, the genome of which expresses a chimeric DNA molecule which encodes a gene product which confers resistance or tolerance to the plant to a fungal pathogen by inhibiting fungal iron metabolism or siderophore production.

ACTIVITY - Fungicidal; Mycocidal; Antibacterial; Antiarthritic; Dermatological; Antiinflammatory.

No biological data given.

MECHANISM OF ACTION - Antisense therapy.

No biological data given.

USE - The polynucleotides and **polypeptides** are useful for identifying a novel fungicidal or mycocidal mode of action which permits rapid discovery of novel inhibitors of gene products that are useful as fungicides or mycocides.

The agents and antisense DNA are useful as fungicides to suppress the growth of pathogenic fungi. The fungal pathogens include plant pathogens such as Septoria trici, or Cochliobolus heterostrophus, or animal pathogens such as Candida albicans.

The anti-fungal agents are particularly useful for treating fungal infections of vertebrates, including immunocompromised vertebrates, for e.g. pneumonia, arthritis, miliary disease, bone and joint infection, skin disease, aesophagitis, vaginitis, onychomycosis, and inflammation of urinary tract, kidney, liver, brain, gastrointestinal tract and lung.

Dwg.0/10

L34 ANSWER 6 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-739924 [80] WPIDS

DOC. NO. NON-CPI: N2002-582921
DOC. NO. CPI: C2002-209497

TITLE: New recombinant spherical outer wall

glycoproteins from Coccidioides immitis,

useful as antigens for serodiagnosis or induction

of an immune response.

DERWENT CLASS: B04 C06 C07 D16 S03 INVENTOR(S): COLE, G T; HUNG, C

PATENT ASSIGNEE(S): (MEDI-N) MEDICAL COLLEGE OHIO

COUNTRY COUNT:

PATENT INFORMATION:

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 20021063	80 Al Provisional	US 2000-202754P US 2001-850677	

PRIORITY APPLN. INFO: US 2000-202754P 20000508; US 2001-850677 20010507

AN 2002-739924 [80] WPIDS

AB US2002106380 A UPAB: 20021212

NOVELTY - A **recombinant** spherical outer wall glycoprotein 58 (SOWqp58) (I) from **Coccidioides** immitis, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

- (1) antigens (II) for serodiagnosis of coccidioidomycosis comprising a recombinant spherical outer wall glycoprotein (SOWgp);
- (2) an isolated nucleic acid (III) that hybridizes under highly stringent conditions to a probe of sequences (S1: 900 base pairs), (S3: 1244 base pairs), (S9: 1504 base pairs) or (S11: 1563 base pairs), or their complements;
- (3) purified **polypeptides** (IV) that comprise sequences (S2: 299 amino acids (aa)), (S4: 328 aa), (S5: 15 aa), (S6: 10 aa), (S7: 10 aa), (S8: 14 aa); (S10: 375 aa) or (S12: 422 aa), all (sic) with up to 20 conservative aa substitutions;
- (4) eliciting (M1) a proliferative response from monocytes, in animals that show a positive skin test, by administering Ag; and
 - (5) identifying (M2) the SOW gp58, gp66 and/or gp82 genes. ACTIVITY Fungicide.

No biological data given.

 ${\tt MECHANISM}$ OF ACTION - Induction of specific humoral and cellular immune responses.

Purified SOWgp58 from the Silveria isolate was tested in an essentially conventional proliferation assay (thymidine incorporation) against peripheral blood mononuclear cells. At a concentration of 50 micro g/ml in the cell culture medium it produced a stimulation index of 16, using cells from subjects who gave a positive skin test for C. immitis, but the index was only about 1 when using cells from subjects who gave a negative skin test.

- $\ensuremath{\mathsf{USE}}$ Spherical outer wall glycoproteins (SOW) are antigens useful for:
- (a) serodiagnosis of **coccidioidomycosis** (San Joaquin Valley fever); and
- (b) for stimulating proliferation of peripheral blood monocytes, for protection against this disease.
- (III) that encode SOW are useful as probes and primers for cloning, and as diagnostic probes. ${\rm Dwg.}\,0/9$

L34 ANSWER 7 OF 18 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2002322692 MEDLINE

DOCUMENT NUMBER: 22060669 PubMed ID: 12065493

TITLE: Role of signal sequence in vaccine-induced protection

against experimental coccidioidomycosis.

AUTHOR: Jiang Chengyong; Magee D Mitchell; Ivey F Douglas;

Cox Rebecca A

CORPORATE SOURCE: Department of Microbiology, University of Texas

Health Science Center at San Antonio, San Antonio,

Texas 78229, USA.

SOURCE: INFECTION AND IMMUNITY, (2002 Jul) 70 (7) 3539-45.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200207

ENTRY DATE: Entered STN: 20020615

Last Updated on STN: 20020731 Entered Medline: 20020730

AB The vaccine efficacy of the gene sequence encoding the signal peptide of the antigen known as antigen 2 or proline-rich antigen (Ag2/PRA), an immunodominant antigen present in the cell wall of the fungal pathogen Coccidioides immitis, was investigated in a murine model of coccidioidomycosis. Expression plasmids for Ag2/PRA(1-18) DNA (signal sequence), Ag2/PRA(19-194) DNA (lacking the signal sequence), and Ag2/PRA(1-194) DNA (full length) were inserted in the pVR1012 vector, and the constructs were used to vaccinate the highly susceptible BALB/c mouse strain. Immunization with the signal gene sequence significantly reduced the fungal burden in the lungs and spleens of mice 12 days after intraperitoneal challenge with a lethal dose of 2,500 C. immitis arthroconidia, to a level comparable to the protection induced in mice immunized with the full-length Ag2/PRA(1-194) DNA. The Ag2/PRA(19-194) gene protected mice but to a significantly lower level than the signal sequence or the full-length Ag2 gene. The immunizing capacity of Ag2/PRA(1-18) was not attributable to a nonspecific immunostimulatory effect of DNA, as evidenced by the fact that mice immunized with a frameshift mutation of Ag2/PRA(1-18) were not protected against challenge. Furthermore, a synthetic peptide corresponding to the translated sequence of Ag2/PRA(1-18) DNA protected mice, albeit at a lower level than the Ag2/PRA(1-18) DNA vaccine. The protection induced with the signal gene vaccine correlated with the production of gamma interferon when splenocytes from Ag2/PRA(1-18)-immunized mice were stimulated with recombinant full-length Ag2 and was not associated with the production of anti-Coccidioides immunoglobulin G antibody. This is the first study to establish that a signal peptide sequence alone, administered as a gene vaccine or synthetic peptide, can induce protective immunity against a microbial pathogen.

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ANSWER 8 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
ACCESSION NUMBER:
                      2001-489080 [53]
                                         WPIDS
DOC. NO. NON-CPI:
                      N2001-361848
DOC. NO. CPI:
                      C2001-146921
TITLE:
                      Identifying genes essential to fungal metabolisms
                      and identifying potential therapeutic agents that
                      target these genes.
DERWENT CLASS:
                      B04 D16 S03
INVENTOR(S):
                      BOONE, C; BUSSEY, H; JIANG, B; ROEMER, T
PATENT ASSIGNEE(S):
                      (ELIT-N) ELITRA PHARM INC
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PATENT NO KIND DATE WEEK LA PG

COUNTRY COUNT: PATENT INFORMATION:

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WO 2001060975 A2 20010823 (200153)* EN 320

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE

DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG

KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ

PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN

YU ZA ZW

AU 2001043204 A 20010827 (200176)
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l292668 A2 20030319 (200322) EN R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK

NL PT RO SE SI TR KR 2002097180 A 20021231 (200330) JP 2003523197 W 20030805 (200353)

370

APPLICATION DETAILS:

PATENT NO KIND	APPLICATION	DATE
WO 2001060975 A2	WO 2001-US5551	20010220
AU 2001043204 A	AU 2001-43204	20010220
EP 1292668 A2	EP 2001-916144	20010220
	WO 2001-US5551	20010220
KR 2002097180 A	KR 2002-710815	20020819
JP 2003523197 W	JP 2001-560347	20010220
	WO 2001-US5551	20010220

FILING DETAILS:

PAT	TENT NO	KIND			PA!	FENT NO
AU	200104320	4 A	Based	on	WO	2001060975
EΡ	1292668	A2	Based	on	WO	2001060975
JΡ	200352319	7 W	Based	on	WO	2001060975

PRIORITY APPLN. INFO: US 2000-183534P 20000218

AN 2001-489080 [53]. WPIDS

AB WO 200160975 A UPAB: 20010919

NOVELTY - Methods for constructing fungal strains useful for identification and validation of gene products as target for therapeutic agents, for identifying and validating gene products as target for therapeutic agents, collections id identified genes and screening assays for the discovery of new drugs, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

- (1) a method (I) of constructing a strain of diploid fungal cells (DFCs) in which both alleles (Als) of a gene are modified and for assembling a collection of DFCs each of which comprises modified Als of a different gene;
- (2) a strain of DFCs comprising modified Als of a gene, wherein the first Al of the gene is inactivated by **recombination** using a gene disruption cassette comprising a nucleotide (Nt) sequence (seq) encoding an expressible selectable marker and the expression of the second Al of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second Al of the gene;
- (3) a collection (III) of diploid fungal strains (II) in which each strain comprises modified Als of a different gene, and all the different genes in the genome of the fungus are modified and represented in the collection;
- (4) a NAM microarray (IV) comprising a plurality of nucleic acid molecules (NAMs) (each NAM comprises a Nt seq that is hybridizable to a target Nt seq selected from 62 defined seqs given in the specification, a Nt seq that is hybridizable to the Nt seq of a gene that is either essential to the growth of a DFC or contributes to the virulence and/or pathogenicity of the DFCs against a host organism;
- (5) a method (V) for identifying a gene that is essential to the metabolism/life cycle of a fungus comprising:

- (a) culturing the DFCs (II) under conditions in which the second Al of the gene is substantially under expressed (expd) or not expd; and
- (b) determining:
- (i) viability of the cells (a loss or reduction of viability as compared to a control indicates that the modified gene is essential to the survival of the fungus);
- (ii) growth of the cells (a loss or reduction of growth of the cells as compared to a control indicates that the modified gene is essential to the growth of the fungus);
- (iii) growth of the cells (a loss or reduction of growth of the cells as compared to a control indicates that the modified gene is essential to the growth of the fungus);
- (iv) viability of the cells (an increase in viability as compared to a control indicates that the modified gene contributes to the resistance of the diploid fungus to the antifungal agent);
- (6) a method (VI) for identifying an antifungal agent that inhibits the growth of a diploid fungus;
- (7) a method (VII) for identifying a therapeutic agent for treatment of a mammalian disease;
- (8) a method (VIII) for correlating changes in the levels of proteins with the inhibition of growth or proliferation of a DFC, comprising:
- (a) generating a first protein expression profile for a control DFC which comprises two wild type Als of the gene;
- (b) culturing DFCs (II) under conditions wherein the second Al of the gene is substantially under expd, not expd or over expd, and generating a second **protein** expression profile for the cultured cells; and
- (c) comparing the first protein expression profile with the second protein expression profile to identify changes in the levels of proteins;
- (9) a method (IX) for correlating changes in the levels of gene transcripts with the inhibition of growth or proliferation of a DFC, comprising:
- (a) generating a transcription profile for a control DFC which comprises two wild type Als of the gene;
- (b) culturing DFCs (II) under conditions wherein the second Al of the gene is substantially under expd, not expd or over expd and generating a second transcription profile for the cultured cells; and
- (c) comparing the first transcription profile with the second transcription profile to identify changes in the levels of gene transcripts;
- (10) a NAM (X) comprising a Nt seq encoding a gene product required for proliferation of Candida albicans (the gene product comprises a defined amino acid seq given in the specification);
- (11) a NAM (XI) comprising a fragment of comprising at least 10 to 100 consecutive Nts; a NAM comprising a Nt seq that hybridizes under stringent condition to a second NAM consisting of:
- (a) a Nt seq selected from the seqs given in the specification; or
- (b) a Nt seq that encodes a **polypeptide** comprising an amino acid seq defined in the specification (the stringent conditions comprises hybridization to filter-bound DNA in 6 multiply sodium chloride sodium citrate (SSC) at about 45 deg. C followed by one or more washes in 0.2 multiply SSC/0.1 % sodium dodecyl sulfate (SDS) at about 50-65 deg. C);

- (12) a NAM (XII) obtained from an organism other than Candida albicans or Saccharomyces cerevisiae comprising a Nt seq having at least 30% identity to a defined seq given in the specification, fragments of at least 25 consecutive Nts, and/or seqs complementary to them as determined using BLAST-N version 2.0 with the default parameters;
- (13) a **vector** (XIII) comprising a promoter operably linked to the NAMs above;
 - (14) a host cell (XIV) containing the vector (XIII);
- (15) a polypeptide (XV) comprising a defined amino acid seq given in the specification;
- (16) a polypeptide (XVI) obtained from an organism other than Candida albicans or Saccharomyces cerevisiae comprising an amino acid seq having at least 30% similarity to an amino acid seq defined in the specification as determined using FASTA version 3.0t78 with the default parameters;
- (17) a fusion protein (XVII) comprising a fragment of a polypeptide fused to a second polypeptide (the fragment comprises at least 6 consecutive residues of a defined amino acid seq given in the specification;
- (18) a method (IXX) of producing a polypeptide, comprising introducing into a cell, a vector comprising a promoter operably linked to a Nt seq encoding a polypeptide comprising a defined amino acid seq given in the specification and culturing the cell so that the Nt seq is expd; and
- (19) a method (XX) of producing a polypeptide, comprising providing a cell which comprises a heterologous promoter operably linked to a Nt seq encoding a polypeptide comprising a defined amino acid seq given in the specification and culturing the cell so that the Nt seq is expd.

Note: Other INDEPENDENT CLAIMS are included but have had to be omitted due to lack of space.

USE - The methods are used to identify agents that may be used in the treatment of fungal infections. $\ensuremath{\mathsf{Dwg.0/6}}$

L34 ANSWER 9 OF 18 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER:

2001248085 MEDLINE

DOCUMENT NUMBER:

21189198 PubMed ID: 11292702

TITLE:

Recombinant urease and urease DNA of

Coccidioides immitis elicit an immunoprotective response against

coccidioidomycosis in mice.

AUTHOR: Li K; Yu CORPORATE SOURCE: Departme

Li K; Yu J J; Hung C Y; Lehmann P F; Cole G T Department of Microbiology and Immunology, Medical

College of Ohio, Toledo, Ohio 43614-5806, USA.

CONTRACT NUMBER: AI19149 (NIAID)

AI37232 (NIAID)

SOURCE:

INFECTION AND IMMUNITY, (2001 May) 69 (5) 2878-87.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200105

ENTRY DATE:

Entered STN: 20010517

Last Updated on STN: 20010517 Entered Medline: 20010510

Coccidioides immitis antigens which stimulate a T helper AΒ cell 1 (Th1) pathway of host immune response are considered to be essential components of a vaccine against coccidioidomycosis Recombinant urease (rURE) and recombinant heat shock protein 60 (rHSP60) of C. immitis were expressed in Escherichia coli and tested as vaccine candidates in BALB/c mice. A synthetic oligodeoxynucleotide which contained unmethylated CpG dinucleotides and was previously shown to enhance a murine Th1 response was used as an immunoadjuvant. T cells isolated from the spleens and lymph nodes of the rURE- and rHSP60-immune mice showed in vitro proliferative responses to the respective recombinant protein, but only those T lymphocytes from rURE-immunized mice revealed markedly elevated levels of expression of selected Th1-type cytokine genes. BALB/c mice immunized subcutaneously with rURE and subsequently challenged by the intraperitoneal (i.p.) route with a lethal inoculum of C. immitis arthroconidia demonstrated a significant reduction in the level of C. immitis infection compared to control animals. rHSP60 was much less effective as a protective antigen. Evaluation of cytokine gene expression in lung tissue and levels of recombinant urease-specific immunoglobulins (immunoglobulin G1 [IgG1] versus IgG2a) in murine sera at 12 days after challenge provided additional evidence that immunization with rURE stimulated a Th1 response to the pathogen. Urease was further evaluated by expression of the URE gene in a mammalian plasmid vector (pSecTag2A.URE) which was used to immunize mice by the intradermal route. In this case, 82% of the vector construct-immunized animals survived more than 40 days after i.p. infection, compared to only 10% of the mice immunized with the vector alone. In addition, 87% of the pSecTag2A.UREimmunized survivors had sterile lungs and spleens. These data support the need for further evaluation of the C. immitis urease as a candidate vaccine against coccidioidomycosis.

L34 ANSWER 10 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2002:223315 BIOSIS DOCUMENT NUMBER: PREV200200223315

TITLE: Replacement of the gene which encodes a major

immunoreactive cell surface antigen and adhesin

(SOWgp) of the human fungal pathogen

Coccidioides immitis.

AUTHOR(S): Hung, C. [Reprint author]; Reichard, U. [Reprint

author]; Yu, J. [Reprint author]; Cole, G. T.

[Reprint author]

CORPORATE SOURCE: Medical College of Ohio, Toledo, OH, USA

SOURCE: Abstracts of the General Meeting of the American

Society for Microbiology, (2001) Vol. 101, pp. 365.

print.

Meeting Info.: 101st General Meeting of the American

Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society of Microbiology.

ISSN: 1060-2011.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 3 Apr 2002

Last Updated on STN: 3 Apr 2002

AB We have previously cloned and expressed a major parasitic cell surface antigen (SOWgp) of C. immitis which, upon immunization elicits both antibody and T cell responses in BALB/c mice. Our data also showed that the recombinant SOWgp has high affinity for laminin and fibronectin of the extracellular matrix (ECM). confirm that the SOWgp functions as an adhesin, the SOWgp gene was deleted by a double, locus-specific crossover event. This resulted in replacement of 1.8-kb fragment of the SOWgp gene with a 3.6-kb DNA construct that encodes a hygromycin resistant gene from the pAN7.1 vector. Results of PCR analysis, Southern hybridization, and immunoblot assays of parasitic cell homogenates of the Dsowgp mutant compared to the parental strain confirmed that the SOWgp gene was replaced and the antigen was no longer produced. This is the first report of a successful targeted gene knockout of C. immitis using the double crossover strategy. Comparative immunoelectron-microscopic examinations of the isolated, crude outer parasitic cell wall fraction of the DELTAsowqp and parental strains showed total loss of patient antibody reactivity with the former. The DELTAsowqp parasitic cells showed 20-50% reduction in their ability to bind to human and murine ECM. Virulence studies of the DELTAsowgp strain in intranasally-challenged BALB/c mice showed 20% survival compared to none in the case of mice challenged with the parental strain. It is apparent that deletion of SOWgp production did not eliminate the ability of the pathogen to cause disease. Preliminary investigations of the influence of recombinant SOWqp on immune murine T cells in vitro suggested that the protein stimulates a dominant Th2 response, demonstrated by elevated levels of IL-5 production. Our hypothesis is that SOWqp has a major impact on disseminated coccidioidal infection by compromising the host immune pathway toward a detrimental Th2 response.

L34 ANSWER 11 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2002:223274 BIOSIS

DOCUMENT NUMBER: PREV200200223274

TITLE: Isolation and characterization of a macrophage

binding protein of Coccidioides

immitis.

AUTHOR(S): Cole, G. T. [Reprint author]; Fradin, C. [Reprint

author]

CORPORATE SOURCE: Medical College of Ohio, Toledo, OH, USA

SOURCE: Abstracts of the General Meeting of the American

Society for Microbiology, (2001) Vol. 101, pp. 356.

print.

Meeting Info.: 101st General Meeting of the American

Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society of Microbiology.

ISSN: 1060-2011.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 3 Apr 2002

Last Updated on STN: 3 Apr 2002

AB Early studies have demonstrated the significance of the interplay between Coccidioides immitis and macrophages during coccidioidomycosis. In this study we report the purification of a liquid expressed at the surface of endospores of

C. immitis which binds to an unknown receptor of a murine macrophage line (IC-21). Cell wall proteins of different stages of the parasitic cycle were labeled with biotin and subjected to beta-mercaptoethanol extraction. A single macrophage plasma membrane binding protein (MBP) with molecular size of 36-kDa was isolated from the endospore extract. The C. immitis MBP was purified and two internal peptides of the trypsin-digested fraction were sequenced. Degenerate primers were designed to PCR amplify a fragment of the MBP gene, and the PCR product was then used to screen a C. immitis genomic library for isolation of the full-length gene. The MBP gene is characterized by an open reading frame of 638 bp, and does not contain any introns. The MBP gene was subcloned into the pET28b expression vector and the recombinant, histidine-tagged fusion protein (rMBP) was produced by transformed E. coli stain BL21(DE3). The rMBP was shown to bind to the surface of both IC-21 cells and resident murine peritoneal macrophages. An in vitro study of temporal expression of the MBP gene during the parasitic cycle was conducted by RT-PCR and Northern blot analyses, and showed that maximum expression occurs at the endosporulation stage. Polyclonal antibody raised in guinea pigs against the rMBP was used for immunoblot analyses of beta-mercaptoethanol extracts of intact parasitic cells, as well as total cell homogenates of the saprobic and parasitic phases of C. immitis. The results showed that the rMBP was present only in beta-mercaptoethanol extracts and homogenates of first generation round cells and endospores. We suggest that the newly-isolated MBP of C. immitis plays a pivotal role in the course of coccidioidal infections.

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L34 ANSWER 12 OF 18 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
                      1999-551417 [46]
ACCESSION NUMBER:
                                        WPIDS
                      2002-606631 [65]; 2003-829776 [77]
CROSS REFERENCE:
                     N1999-407989
DOC. NO. NON-CPI:
DOC. NO. CPI:
                      C1999-161024
TITLE:
                      Novel chitin-binding fragments of human chitinase
                      used to treat fungal infections in animals.
DERWENT CLASS:
                      B04 C06 D16 S03
                      GRAY, P W; TJOELKER, L W
INVENTOR(S):
                     (ICOS-N) ICOS CORP
PATENT ASSIGNEE(S):
COUNTRY COUNT:
                      86
PATENT INFORMATION:
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PATENT NO KIND DATE
                       WEEK
WO 9946390 A1 19990916 (199946) * EN
                                        83
   RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
      MW NL OA PT SD SE SL SZ UG ZW
   W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES
       FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK
       LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG
       SI SK SL TJ TM TR TT UA UG UZ VN YU ZW
AU 9929989
            A 19990927 (200006)
             A 20001121 (200065)
BR 9908724
NO 2000004522 A 20001101 (200065)
EP 1078073 A1 20010228 (200113) EN
    R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
US 6200951
             B1 20010313 (200120)
CZ 2000003308 A3 20010711 (200147)
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HU 2001001078 A2 20010730 (200157)
SK 2000001354 A3 20010710 (200157)
MX 2000008863 A1 20010301 (200170)
JP 2002505882 W 20020226 (200219) 86
CN 1357046 A 20020703 (200265)
AU 763582 B 20030724 (200355)
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APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9946390	A1	WO 1999-US5343	
AU 9929989	A	AU 1999-29989	
BR 9908724	А	BR 1999-8724	19990312
		WO 1999-US5343	19990312
NO 2000004	522 A	WO 1999-US5343	19990312
		NO 2000-4522	20000911
EP 1078073	A1	EP 1999-911320	19990312
		WO 1999-US5343	19990312
US 6200951	B1	US 1998-39198	19980312
CZ 2000003	308 A3	WO 1999-US5343	19990312
		CZ 2000-3308	19990312
HU 2001001	078 A2	WO 1999-US5343	19990312
		HU 2001-1078	19990312
SK 2000001	354 A3	WO 1999-US5343	19990312
		SK 2000-1354	19990312
MX 20000088	863 A1	MX 2000-8863	20000911
JP 20025058	882 W	WO 1999-US5343	19990312
		JP 2000-535757	19990312
CN 1357046	A	CN 1999-805990	19990312
AU 763582	В	AU 1999-29989	19990312

FILING DETAILS:

PATENT NO K	IND	PATENT NO
AU 9929989 BR 9908724 EP 1078073 CZ 2000003308 HU 2001001078 SK 2000001354 JP 2002505882	A2 Based on A3 Based on	WO 9946390 WO 9946390 WO 9946390 WO 9946390 WO 9946390 WO 9946390
	B Previous Pu	abl. AU 9929989
	Based on	WO 9946390

PRIORITY APPLN. INFO: US 1998-39198 19980312

AN 1999-551417 [46] WPIDS

CR 2002-606631 [65]; 2003-829776 [77]

AB WO 9946390 A UPAB: 20031128

NOVELTY - Novel human chitinase **polypeptide** and polynucleotide fragments have chitin-binding activity but lack chitinase enzymatic activity.

DETAILED DESCRIPTION - A chitin-binding, chitinase-inactive polypeptide (I) comprises a chitin-binding fragment of the 54 C-terminal amino acids (aa) of human chitinase having a 466 aa sequence (S1) (given in the specification).

INDEPENDENT CLAIMS are also included for the following:

- (1) a chitin-binding, chitinase-inactive polypeptide comprising as residues X-Y of (S1), where X is a consecutive integer from 347 to 397 and Y is 445;
- (2) a fusion protein comprising (I) fused to a heterologous polypeptide (e.g. an enzyme);
- (3) a composition comprising (I) and a diluent, optionally further comprising a non-chitinase anti-fungal agent;
- (4) a composition comprising (I) or the fusion protein of (1) conjugated to an anti-fungal agent;
- (5) treating fungal infection, comprising administering to a subject suffering from fungal infection the composition of (3) or (4), optionally further comprising administering a non-chitinase anti-fungal agent;
- (6) a composition comprising (I) or the fusion protein of (1) conjugated to a detectable label, especially radioisotopes, fluorophores, dyes, electron-dense compounds or enzymes;
- (7) determining the presence of chitin in a sample, comprising contacting the sample with the composition of (6), and determining the amount of labelled polypeptide bound to chitin;
- (8) a purified, isolated polynucleotide (especially DNA) encoding (I);
 - (9) a vector comprising the DNA of (8);
- (10) a host cell stably transformed or transfected with the DNA of (8) in a manner allowing the expression of (I), and
- (11) a monoclonal antibody that specifically binds to an epitope within the 54 C-terminal amino acids of human chitinase having a sequence (S1).

ACTIVITY - Chitin-binding.

MECHANISM OF ACTION - None given.

USE - Chitinase fragments can be used to screen for proteins or other molecules that specifically bind to the chitin-binding domain of human chitinase or that modulate its activity. These compounds are useful for immunization, as well as for purifying chitinase, as well as for detection and quantification of chitinase. Polynucleotide fragments of the invention are useful as a source of probes and primers, and to express the proteins recombinantly. The chitinase fragments, when conjugated to antifungal compounds, are used to treat animals, especially humans, infected with chitin-containing parasites such as fungi. Fungal infection treated include candidiasis, aspergillosis, coccidioidomycosis, blastomycosis, paracoccidioidomycosis, mucormycosis, histoplasmosis, cryptococcosis, chromoblastomycosis, sporotrichosis, and dermatophytoses.

ADVANTAGE - Chitin can be degraded by the enzyme chitinase. Use of whole chitinase protein for treating infections, especially fungal infections, is problematic. In view of the increasing incidences of life- threatening fungal infection in e.g. immunocompromised individuals, there exists a need fro identifying new compounds for treating fungal infection. The chitin-binding fragments of the present invention provide this need. Dwg.0/0

L34 ANSWER 13 OF 18

MEDLINE on STN

DUPLICATE 4

ACCESSION NUMBER: 1999085554 DOCUMENT NUMBER:

MEDLINE

TITLE:

99085554 PubMed ID: 9868663 Detecting serum antibodies to a purified

recombinant proline-rich antigen of Coccidioides immitis in patients with

Shears 308-4994 Searcher :

coccidioidomycosis.

AUTHOR: Orsborn K I; Galgiani J N

CORPORATE SOURCE: Research and Medical Services, Veterans Affairs

Medical Center, Tucson, Arizona, USA.

SOURCE: CLINICAL INFECTIOUS DISEASES, (1998 Dec) 27 (6)

1475-8.

Journal code: 9203213. ISSN: 1058-4838.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990324

Last Updated on STN: 19990324 Entered Medline: 19990308

AB In previous work, antibodies in serum samples from patients with coccidioidomycosis were found to react with a proline-rich antigen (PRA) isolated from spherules of Coccidioides immitis, and the gene encoding this antigen was cloned. expressed and purified recombinant PRA (rPRA) by removing the majority of amino acids contributed by the vector from the fusion protein. Purified rPRA reacted with serum IgG antibodies in 37 of 42 patients with culture-proven progressive pulmonary or extrapulmonary coccidioidal disease; specific antibodies in dilutions ranging from 1:40 to 1:102,400 were demonstrated (sensitivity, 88%). In contrast, for > 95% of patients without coccidioidomycosis reactivity of < 1:40 was demonstrated (specificity, 97%). Of 18 patients with primary self-limited coccidioidomycosis, none had detectable antibodies in serum samples collected up to 141 days after illness began. The association of antibodies to rPRA with progressive infection may have prognostic value.

L34 ANSWER 14 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on

STN

ACCESSION NUMBER: 1997:500830 BIOSIS DOCUMENT NUMBER: PREV199799800033

TITLE: Isolation and characterization of the urease gene

(URE) from the pathogenic fungus Coccidioides

immitis.

AUTHOR(S): Yu, Jieh-Juen; Smithson, S. L.; Thomas, Pei W.;

Kirkland, Theo N.; Cole, Garry T. [Reprint author]

CORPORATE SOURCE: Dep. Microbiol. Immunol., Med. Coll. Ohio, 3000

Arlington Ave., Toledo, OH 43699, USA

SOURCE: Gene (Amsterdam), (1997) Vol. 198, No. 1-2, pp.

387-391.

CODEN: GENED6. ISSN: 0378-1119.

DOCUMENT TYPE: Article LANGUAGE: English

ENTRY DATE: Entered STN: 21 Nov 1997

Last Updated on STN: 21 Nov 1997

AB The urease (URE)-encoding gene from **Coccidioides** immitis (Ci), a respiratory fungal pathogen of humans, was cloned, sequenced, chromosome-mapped and expressed. Both the genomic and cDNA sequences are reported. The transcription start point and poly(A)-addition site were confirmed. The URE gene contains eight introns and a 2517-bp ORF that translates a 839-amino-acid (aa) **protein** of 91.5 kDa and pI of 5.5, as deduced by computer

analysis of the nucleotide sequence. The translated **protein** revealed eight putative N-glycosylation sites. The deduced URE showed comparable levels of homology to reported URE of the jack bean plant (Canavalia ensiformis; 71.8%) and URE of several genera of bacteria (Bp, 71.7%; Hp, 68.3%; Ka, 71.6%; Pm, 71.9%). The URE gene was mapped to chromosome III of Ci and was shown to be a single copy gene by Southern hybridization. Expression of a 1687-bp fragment of the URE gene in E. coli resulted in the production of a 63-kDa **recombinant protein** that was recognized in an immunoblot by antiserum raised against the Ka URE homolog. This is the first report of a fungal URE gene.

L34 ANSWER 15 OF 18 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 96294782 MEDLINE

DOCUMENT NUMBER: 96294782 PubMed ID: 8698497

TITLE: Molecular cloning and characterization of

Coccidioides immitis antigen 2 cDNA.

AUTHOR: Zhu Y; Yang C; Magee D M; Cox R A

CORPORATE SOURCE: Department of Clinical Investigation, Texas Center

for Infectious Disease, San Antonio 78223, USA.

CONTRACT NUMBER: AI2143 (NIAID)

SOURCE: INFECTION AND IMMUNITY, (1996 Jul) 64 (7) 2695-9.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals OTHER SOURCE: GENBANK-U32518

ENTRY MONTH: 199609

ENTRY DATE: Entered STN: 19960912

Last Updated on STN: 19960912 Entered Medline: 19960904

AB Previous experiments have provided evidence that **Coccidioides** immitis antigen 2 (Ag2) is a major

T-cell-reactive component of mycelia and spherule cell walls. we report the identification and cloning of the cDNA that encodes Ag2 from a lambda ZAP cDNA expression library constructed from spherule-derived RNA. DNA sequence analysis established that the 1,255-bp clone contains a 174-bp 5' untranslated region, a 582-bp open reading frame which encodes for a protein consisting of 194 amino acids, and a 375-bp 3' untranslated region, including a poly(A) tail. The recombinant Ag2 protein has a predicted molecular mass of 19.5 kDa and contains an 18-amino-acid N terminus which has been tentatively identified as a signal peptide. The Ag2 cDNA was ligated into the pGEX-4T-3 vector and expressed in Escherichia coli TG-1 cells as a glutathione S-transferase fusion protein. The recombinant fusion protein showed reactivity with sera from patients with coccidioidomycosis and elicited delayed-type footpad hypersensitivity responses in Coccidioides-immune mice. These results suggest that the Aq2 cDNA can be used for the large-scale production of this immunologically important protein.

L34 ANSWER 16 OF 18 MEDLINE on STN DUPLICATE 6

ACCESSION NUMBER: 96239008 MEDLINE

DOCUMENT NUMBER: 96239008 PubMed ID: 8675298

TITLE: Molecular cloning and characterization of the

Coccidioides immitis complement

fixation/chitinase antigen.

AUTHOR: Yang C; Zhu Y; Magee D M; Cox R A

CORPORATE SOURCE: Department of Clinical Investigation, Texas Center

for Infectious Diseases, San Antonio, 78223, USA.

CONTRACT NUMBER: AI 12431 (NIAID)

SOURCE:

INFECTION AND IMMUNITY, (1996 Jun) 64 (6) 1992-7.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals GENBANK-U33265 OTHER SOURCE:

ENTRY MONTH: 199608

ENTRY DATE: Entered STN: 19960822

> Last Updated on STN: 19960919 Entered Medline: 19960812

AΒ Detection of anti-Coccidioides complement-fixing (CF) antibody is a valuable diagnostic and prognostic aid in coccidioidomycosis. The CF antibody response is directed against a heat-labile antigen that has chitinase activity, hereafter referred to as the CF/chitinase protein. To identify and clone this immunoreactive enzyme, we constructed a Coccidioides immitis cDNA lambda ZAP expression library from spherule RNA and detected fusion peptides expressing CF epitopes by inmunoscreening. A cDNA clone consisting of 1,623 bp was identified, sequenced, and found to contain a single open reading frame that encodes a protein of 47 kDa with 427 amino acids. Deduced amino acid sequence analyses showed that the cloned CF/chitinase cDNA contains a 35-amino-acid region, beginning at Ser-18 and ending at and ending at Arg-52 which has 92% homology with the reported N-terminal amino acid sequence of authentic CF/chitinase protein. The first 17 amino acids in the deduced sequence of the cloned cDNA are not present on the mature CF/chitinase protein, suggesting that it may be a signal peptide. Expression of the CF/chitinase cDNA insert by using the pGEX-4T-3 vector yields a fusion peptide that bears CF-specific epitopes and shows chitinase activity. CF/chitinase clone will enable large-scale production of the recombinant CF antigen for use in immunoassays and facilitate studies on the role of chitinase in the morphogenesis of

L34 ANSWER 17 OF 18 MEDLINE on STN DUPLICATE 7

ACCESSION NUMBER: 96009757 MEDLINE

PubMed ID: 7558310 DOCUMENT NUMBER: 96009757

Molecular and biochemical characterization of a TITLE:

Coccidioides immitis-specific antigen.

AUTHOR: Pan S; Cole G T

Department of Microbiology, Medical College of Ohio, CORPORATE SOURCE:

Toledo 43699-0008, USA.

AI19149 (NIAID) CONTRACT NUMBER:

INFECTION AND IMMUNITY, (1995 Oct) 63 (10) 3994-4002. Journal code: 0246127. ISSN: 0019-9567. SOURCE:

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

C. immitis.

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-L36551

ENTRY MONTH: 199510

ENTRY DATE: Entered STN: 19951227

Last Updated on STN: 19951227 Entered Medline: 19951030

AΒ Results of earlier investigations have indicated that the saprobic phase of Coccidioides immitis produces a heat-stable, 19-kDa antigen with serine proteinase activity which has been suggested to be specific for this pathogenic fungus. In the present study we have determined the N-terminal and partial internal amino acid sequences of the purified, 19-kDa antigen, cloned the gene which encodes this polypeptide, and confirmed that the secreted proteinase is a Coccidioides-specific antigen (CS-Ag). Both the genomic and cDNA sequences are reported and reveal that the csa gene which encodes this antigen has no introns. A 543-bp open reading frame encodes a 181-amino-acid-containing protein with a predicted molecular mass of 19.8 kDa and an isoelectric point of 8.3. The csa gene was localized on chromosome I of three representative C. immitis clinical isolates on the basis of Southern hybridizations. Expression of the csa gene in Escherichia coli using the pET21a plasmid vector yielded a recombinant protein that was recognized in immunoblot assays by antibody raised to the purified 19-kDa CS-Aq. Secretion of the native antigen is suggested to occur by cleavage of a putative 23-residue signal **peptide**. The native CS-Ag showed a low degree of glycosylation. Analysis of the carbohydrate composition of the CS-Ag revealed xylose, mannose, galactose, and glucose. However, the purified antigen showed no affinity for concanavalin A. A PCR method with specificity and high sensitivity for detection of C. immitis genomic DNA, using a pair of synthetic oligonucleotide primers whose sequences were based on that of the csa gene, was developed. A 520-bp product was amplified only when C. immitis genomic DNA was used as the template. The lower limits of DNA detection using this PCR method were 1 pg of C. immitis genomic DNA by ethidium bromide staining and 100 fg after Southern hybridization. The csa gene-based PCR method for detection of C. immitis DNA is useful for culture identification and may have clinical applications for the diagnosis of coccidioidal infections.

L34 ANSWER 18 OF 18 MEDLINE ON STN ACCESSION NUMBER: 94129182 MEDLINE

DOCUMENT NUMBER: 94129182 PubMed ID: 8298279

TITLE: Identification of antigens of **Coccidioides** immitis which stimulated immune T lymphocytes.

AUTHOR: Cole G T; Kirkland T N

CORPORATE SOURCE: Department of Botany, University of Texas, Austin

78713.

CONTRACT NUMBER: AI19149 (NIAID)

SOURCE: ARCHIVES OF MEDICAL RESEARCH, (1993 Autumn) 24 (3)

281-91.

Journal code: 9312706. ISSN: 0188-4409.

PUB. COUNTRY: Mexico

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199403

ENTRY DATE: Entered STN: 19940318

Last Updated on STN: 19940318 Entered Medline: 19940308

AB T-cell mediated immune response to coccidioidomycosis has been shown to be the principal mechanism of resistance to this respiratory fungal disease in experimental animals. In this study, a Coccidioides immitis antigen-specific murine T-cell line was used to identify macromolecules capable of eliciting an immune mouse T-cell proliferative response. The murine T-cell line was selected on the basis of its strong positive response to a soluble conidial wall fraction (SCWF), which had previously been shown to be reactive in humoral and cellular immunoassays. An antigen-specific T-cell line rather than T-cell clones was used to identify multiple antigens. The T-cell immunoblot method was employed first to identify immunoreactive sub-fractions of the SCWF, and then to identify T-cell fusion proteins (FPs) obtained from a cDNA expression library constructed in lambda gtll. The library was screened with anti-SCWF. The nucleotide sequence of a 0.2 kilobase cDNA insert encoding a FP which elicited vigorous T-cell response was determined. A construct of this insert was subcloned into the pET expression vector system and 6.5-kilodalton (kDa) recombinant protein (RP) expressed in Escherichia coli was isolated. The RP and FP were shown to be homologous on the basis of identify of their amino acid sequences. Antibody raised in guinea pigs against the RP recognized a 59-kDa native protein of the mycelial culture filtrate produced by three separate strains of C. immitis, and reacted with the cell wall of arthroconidia as detected by immunofluorescence microscopy. In this study we have identified and partly characterized a potentially important T-cell stimulating antigen of C. immitis.

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(FILE 'MEDLINE' ENTERED AT 09:35:53 ON 04 DEC 2003)

L35 720 SEA FILE=MEDLINE ABB=ON PLU=ON COCCIDIOIDES/CT

L36 120410 SEA FILE=MEDLINE ABB=ON PLU=ON PROTEINS/CT

L37 86 SEA FILE=MEDLINE ABB=ON PLU=ON POLYPROTEINS/CT

L38 73063 SEA FILE=MEDLINE ABB=ON PLU=ON PEPTIDES/CT

L39 7 SEA FILE=MEDLINE ABB=ON PLU=ON L35 AND (L36 OR L37 OR L38)
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- L39 ANSWER 1 OF 7 MEDLINE on STN
- AN 2002322678 MEDLINE
- TI Localization within a proline-rich antigen (Ag2/PRA) of protective antigenicity against infection with Coccidioides immitis in mice.
- AU Peng Tao; Shubitz Lisa; Simons Julie; Perrill Robert; Orsborn Kris I; Galgiani John N
- SO INFECTION AND IMMUNITY, (2002 Jul) 70 (7) 3330-5. Journal code: 0246127. ISSN: 0019-9567.
- AB Subunits of a proline-rich coccidioidal antigen (Ag2/PRA) of Coccidioides immitis were analyzed by comparison as vaccines in mice. The optimal dose of plasmid vaccine encoding full-length Ag2/PRA was determined to be between 10 and 100 microg. Mice vaccinated with plasmids encoding amino acids (aa) 1 to 106 were as protective as full-length Ag2/PRA (aa 1 to 194). The subunit from aa 27 to 106 was significantly but less protective. Plasmids encoding aa 90 to 151 or aa 90 to 194 were not protective. Analogous results were obtained with recombinant vaccines of the same amino acid sequences. In addition, mixtures of aa 90 to 194 with either aa 1 to 106 or aa 27 to 106 did not enhance protection compared to the active single-recombinant subunits alone. Humoral

response of total immunoglobulin G (IgG) and subclasses IgG1 and IgG2a were detectable in subunit vaccinations but at significantly (100-fold) lower concentrations than after vaccination with plasmids encoding full-length Ag2/PRA. Since virtually all protection by vaccination with full-length Ag2/PRA can be accounted for in the first half of the protein (aa 1 to 106), this subunit could make a multicomponent vaccine more feasible by reducing the quantity of protein per dose and the possibility of an untoward reactions to a foreign protein.

- L39 ANSWER 2 OF 7 MEDLINE on STN
- AN 1999094977 MEDLINE
- TI Proline-rich vaccine candidate antigen of Coccidioides immitis: conservation among isolates and differential expression with spherule maturation.
- AU Peng T; Orsborn K I; Orbach M J; Galgiani J N
- SO JOURNAL OF INFECTIOUS DISEASES, (1999 Feb) 179 (2) 518-21. Journal code: 0413675. ISSN: 0022-1899.
- AB A proline rich antigen (PRA), which protects mice against Coccidioides immitis, has been analyzed for differential expression and variation among isolates. Northern blots of RNA from different stages of growth were probed with previously cloned cDNA and showed that mRNA for PRA increased as spherules transformed and matured from mycelia. This pattern corresponds to the relative potency of whole cell vaccines from similar preparations. The PRA gene was then cloned from a genomic library of the Silveira strain of C. immitis and its sequence analyzed. Eight other coccidioidal isolates, selected for diversity in geographic origin and resulting clinical disease, demonstrated heterogeneity in Southern blots and in sequences of polymerase chain reaction products. Silveira differed from other California isolates at 33 of 555 bases, whereas it differed from non-California isolates by <=2 bases. Only one of these substitutions affected protein sequence. Thus, tests or vaccines based on this gene are likely to cover most isolates.
- L39 ANSWER 3 OF 7 MEDLINE on STN
- AN 96144702 MEDLINE
- TI Cloning and sequence analysis of the cDNA for a protein from Coccidioides immitis with immunogenic potential.
- AU Dugger K O; Villareal K M; Ngyuen A; Zimmermann C R; Law J H; Galgiani J N
- SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1996 Jan 17) 218 (2) 485-9.

 Journal code: 0372516. ISSN: 0006-291X.
- AB We have cloned and sequenced the cDNA encoding an immunoreactive protein from the pathogenic fungus Coccidioides immitis which stimulates human T cells and has been associated with protective vaccines in mice. The transcript contained an open reading frame encoding 194 amino acids with a calculated molecular weight of 19.5 kDa, a 151 base 5' untranslated region (UTR), and a 468 base 3'UTR. A four member repeat motif, usually thr-ala-glu-pro, exists for amino acids 98 through 141. Deduced amino acid sequence derived from the cDNA was identical with previously determined internal amino acid sequence from the native protein, and goat antiserum raised against the purified fungal protein reacted with an inducible fusion protein translated from this cDNA. Using this cDNA to produce recombinant protein will allow direct testing of its role in human immunity to coccidioidomycosis and may lead to new diagnostic

tests.

- L39 ANSWER 4 OF 7 MEDLINE on STN
- AN 90383461 MEDLINE
- TI Activity of cilofungin against Coccidioides immitis: differential in vitro effects on mycelia and spherules correlated with in vivo studies.
- AU Galgiani J N; Sun S H; Clemons K V; Stevens D A
- SO JOURNAL OF INFECTIOUS DISEASES, (1990 Oct) 162 (4) 944-8. Journal code: 0413675. ISSN: 0022-1899.
- AB Cilofungin, a new antifungal drug, was found to inhibit mycelial growth of Coccidioides immitis. Light and electron microscopic observations indicated delay in development of the outer hyphal wall. Cilofungin also blocked incorporation of the chitin substrate, N-acetylglucosamine, into mycelia. However, when C. immitis was grown under conditions that induced spherule development, drug effects were dramatically decreased. Furthermore, efficacy of cilofungin in treatment of murine coccidioidomycosis could not be demonstrated. These studies indicate that glucan-synthase inhibitors have activity against C. immitis, and other compounds with different pharmacologic properties or in combination with other antifungal drugs may exploit this biologic effect.
- L39 ANSWER 5 OF 7 MEDLINE on STN
- AN 75150364 MEDLINE
- TI Immunocompetence and prognosis in patients with gynecologic cancer.
- AU Nalick R H; Disaia P J; Rea T H; Morrow C P
- SO GYNECOLOGIC ONCOLOGY, (1974 Apr) 2 (1) 81-92. Journal code: 0365304. ISSN: 0090-8258.
- L39 ANSWER 6 OF 7 MEDLINE on STN
- AN 72041293 MEDLINE
- TI Fractionation and composition studies of skin test-active components of sensitins from Coccidioides immitis.
- AU Anderson K L; Wheat R W; Conant N F
- SO APPLIED MICROBIOLOGY, (1971 Sep) 22 (3) 294-9. Journal code: 7605802. ISSN: 0003-6919.
- L39 ANSWER 7 OF 7 MEDLINE on STN
- AN 68239308 MEDLINE
- TI Sarcoidosis. II. A clinical evaluation of the alteration in delayed hypersensitivity.
- AU Lordon R E; Young R L; Shapiro S S; Smith R E; Weg J G
- SO AMERICAN REVIEW OF RESPIRATORY DISEASE, (1968 Jun) 97 (6) 1009-16. Journal code: 0370523. ISSN: 0003-0805.
 - (FILE 'HCAPLUS' ENTERED AT 09:41:53 ON 04 DEC 2003)
- L52 208 SEA FILE=HCAPLUS ABB=ON PLU=ON C IMMITIS
- L53 74 SEA FILE-HCAPLUS ABB=ON PLU=ON L52 AND (PROTEIN OR POLYPEPTIDE OR PROTEIN OR PEPTIDE)
- L54 10 SEA FILE=HCAPLUS ABB=ON PLU=ON L53 AND VECTOR
- L55 7 SEA FILE=HCAPLUS ABB=ON PLU=ON L54 AND RECOMBIN?
- L56 0 L55 NOT L32

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,

JICST-EPLUS, JAPIO' ENTERED AT 09:43:13 ON 04 DEC 2003) L57 22 S L55 0 S L57 NOT L33 L58 (FILE 'USPATFULL' ENTERED AT 09:44:23 ON 04 DEC 2003) L59 635 SEA FILE-USPATFULL ABB-ON PLU-ON (COCCIDIOD? OR C) (W) IMMITIS OR COCCIDIOIDOMYC? L60 4 SEA FILE-USPATFULL ABB-ON PLU-ON L59(10A) (PROTEIN OR PEPTIDE OR POLYPEPTIDE OR POLYPROTEIN) L59 635 SEA FILE=USPATFULL ABB=ON PLU=ON (COCCIDIOD? OR C) (W) IMMITIS OR COCCIDIOIDOMYC? L65 246 SEA FILE-USPATFULL ABB-ON PLU-ON L59(S) (PROTEIN OR PEPTIDE OR POLYPEPTIDE OR POLYPROTEIN) L66 2 SEA FILE=USPATFULL ABB=ON PLU=ON L65(S)(VECTOR(3A)RECOM BIN?) 6 L60 OR L66 L67 L67 ANSWER 1 OF 6 USPATFULL on STN ACCESSION NUMBER: 2003:311860 USPATFULL TITLE: Glucanosyl transferase-1 protein useful for immunization against Coccidioides spp. INVENTOR(S): Cole, Garry T., Toledo, OH, UNITED STATES Delgado, Nelson, Delran, NJ, UNITED STATES Yu, Jieh-Juen, Toledo, OH, UNITED STATES Xue, Jianmin, Toledo, OH, UNITED STATES NUMBER KIND DATE US 2003219455 A1 20031127 US 2003-417997 A1 20030416 (10) PATENT INFORMATION: APPLICATION INFO.: NUMBER DATE US 2002-374152P 20020422 (60) PRIORITY INFORMATION: DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION LEGAL REPRESENTATIVE: Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San Francisco, CA, 94105-2482 NUMBER OF CLAIMS: 52 EXEMPLARY CLAIM: 1 NUMBER OF DRAWINGS: 4 Drawing Page(s) LINE COUNT: 2165 AΒ The present invention provides compositions of $1,3-\beta$ -glucanosyltransferase (Gel-1) antigens and polynucleotides encoding the Gel-1 antigens, which Gel-1 antigens are useful for generating an immunological response in an individual and in therapeutic and diagnostic applications of infections due to pathogenic Coccidioides spp. fungi, such as C. immitis or C. posadasii. INCL INCLM: 424/190.100 INCLS: 435/069.300; 435/070.210; 435/252.300; 435/320.100;

Searcher: Shears 308-4994

530/350.000; 536/023.700

NCL NCLM: 424/190.100

> NCLS: 435/069.300; 435/070.210; 435/252.300; 435/320.100;

> > 530/350.000; 536/023.700

L67 ANSWER 2 OF 6 USPATFULL on STN

ACCESSION NUMBER:

PATENT INFORMATION: APPLICATION INFO .: RELATED APPLN. INFO.: 2003:258639 USPATFULL

TITLE:

INVENTOR(S):

207 human secreted proteins Ni, Jian, Germantown, MD, UNITED STATES

Ebner, Reinhard, Gaithersburg, MD, UNITED STATES LaFleur, David W., Washington, DC, UNITED STATES Moore, Paul A., Germantown, MD, UNITED STATES Olsen, Henrik S., Gaithersburg, MD, UNITED STATES Rosen, Craig A., Laytonsville, MD, UNITED STATES Ruben, Steven M., Olney, MD, UNITED STATES Soppet, Daniel R., Centreville, VA, UNITED STATES Young, Paul E., Gaithersburg, MD, UNITED STATES

Shi, Yanggu, Gaithersburg, MD, UNITED STATES Florence, Kimberly A., Rockville, MD, UNITED

STATES

Wei, Ying-Fei, Berkeley, CA, UNITED STATES Florence, Charles, Rockville, MD, UNITED STATES Hu, Jing-Shan, Mountain View, CA, UNITED STATES Li, Yi, Sunnyvale, CA, UNITED STATES Kyaw, Hla, Frederick, MD, UNITED STATES Fischer, Carrie L., Burke, VA, UNITED STATES Ferrie, Ann M., Painted Post, NY, UNITED STATES Fan, Ping, Potomac, MD, UNITED STATES Feng, Ping, Gaithersburg, MD, UNITED STATES Endress, Gregory A., Florence, MA, UNITED STATES Dillon, Patrick J., Carlsbad, CA, UNITED STATES

Carter, Kenneth C., North Potomac, MD, UNITED STATES Brewer, Laurie A., St. Paul, MN, UNITED STATES

Yu, Guo-Liang, Berkeley, CA, UNITED STATES Zeng, Zhizhen, Lansdale, PA, UNITED STATES Greene, John M., Gaithersburg, MD, UNITED STATES

NUMBER	KIND	DATE	
US 2003181692 US 2001-933767		20030925	(0)
Continuation-in-p	oart of	Ser. No.	V = V

filed on 21 Feb 2001, PENDING

Continuation-in-part of Ser. No. US 1998-205258,

filed on 4 Dec 1998, PENDING

		 NUMBER	DATE	
PRIORITY	INFORMATION:	 -49375P -48881P -48880P -48896P -49020P -48876P	20000224 20000329 19970606 19970606 19970606 19970606 19970606 19970606	(60)

\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	1997-48884P 1997-48894P 1997-48964P 1997-48893P 1997-48893P 1997-48900P 1997-48901P 1997-48915P 1997-48915P 1997-48970P 1997-48970P 1997-48973P 1997-48973P 1997-48974P 1997-48974P 1997-48974P 1997-4883P 1997-4883P 1997-4883P 1997-48875P 1997-48875P 1997-48875P 1997-48875P 1997-48875P 1997-48876P 1997-5766P 1997-5764P 1997-5764P 1997-5764P 1997-5764P 1997-5764P 1997-5764P	19970606 (60) 19970905 (60) 19970905 (60)
US	1997-57648P	19970905 (60)
US	1997-57774P	19970905 (60)

US 1997-57776P 19970905 (60) US 1997-57778P 19970905 (60) US 1997-57629P 19970905 (60) US 1997-57628P 19970905 (60) US 1997-57777P 19970905 (60) US 1997-57634P 19970905 (60) US 1997-70923P 19971218 (60) US 1998-92921P 19980715 (60) US 1998-94657P 19980730 (60) US 1997-70923P 19971218 (60) US 1998-92921P 19980715 (60) US 1998-94657P 19980730 (60) Utility APPLICATION ROCKVILLE, MD, 20850 23

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE,

NUMBER OF CLAIMS: 2: EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 10 Drawing Page(s)

LINE COUNT: 32746

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating diseases, disorders, and/or conditions related to these novel human secreted proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 536/023.100

INCLS: 530/350.000; 435/325.000; 435/183.000; 435/069.100;

435/320.100

NCL NCLM: 536/023.100

NCLS: 530/350.000; 435/325.000; 435/183.000; 435/069.100;

435/320.100

L67 ANSWER 3 OF 6 USPATFULL on STN

ACCESSION NUMBER: 2003:127198 USPATFULL

TITLE: Death associated kinase containing ankyr in

repeats (DAKAR) and methods of use

INVENTOR(S): Bird, Timothy A., Bainbridge Island, WA, UNITED

STATES

Holland, Pamela M., Seattle, WA, UNITED STATES Peschon, Jacques J., Seattle, WA, UNITED STATES Virca, George D., Bellevue, WA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION: APPLICATION INFO.:	US 2003087411 US 2002-164080		20030508	(10)

NUMBER DATE

PRIORITY INFORMATION: US 2001-295959P 20010604 (60) US 2001-334362P 20011129 (60)

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: IMMUNEX CORPORATION, LAW DEPARTMENT, 51

UNIVERSITY STREET, SEATTLE, WA, 98101

NUMBER OF CLAIMS: 16 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 4 Drawing Page(s)

LINE COUNT: 5574

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention relates to DAKAR, a new member of the serine/threonine kinase family, methods of making such polypeptides, and to methods of using them to treat conditions associated with apoptosis and epithelial proliferation and differentiation, as well as methods to identify compounds that alter DAKAR-associated cellular activities.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 435/194.000

INCLS: 435/069.100; 435/320.100; 435/325.000; 536/023.200

NCL NCLM: 435/194.000

NCLS: 435/069.100; 435/320.100; 435/325.000; 536/023.200

L67 ANSWER 4 OF 6 USPATFULL on STN

ACCESSION NUMBER: 2003:38356 USPATFULL

TITLE: 125 human secreted proteins

INVENTOR(S): Rosen, Craig A., Laytonsville, MD, UNITED STATES

Feng, Ping, Gaithersburg, MD, UNITED STATES Ruben, Steven M., Olney, MD, UNITED STATES

Ebner, Reinhard, Gaithersburg, MD, UNITED STATES Olsen, Henrik S., Gaithersburg, MD, UNITED STATES

Ni, Jian, Germantown, MD, UNITED STATES Wei, Ying-Fei, Berkeley, CA, UNITED STATES

Soppet, Daniel R., Centreville, VA, UNITED STATES

Moore, Paul A., Germantown, MD, UNITED STATES

Kyaw, Hla, Frederick, MD, UNITED STATES

LaFleur, David W., Washington, DC, UNITED STATES Shi, Yanggu, Gaithersburg, MD, UNITED STATES

Janat, Fouad, Westerly, RI, UNITED STATES

Endress, Gregory A., Florence, MA, UNITED STATES Carter, Kenneth C., North Potomac, MD, UNITED

DATE

STATES

Birse, Charles E., North Potomac, MD, UNITED

KIND

1998-US23435, filed on 4 Nov 1998, UNKNOWN

STATES

PATENT INFORMATION:	US 2003028003	A1	20030206
APPLICATION INFO.:	US 2001-974879	A1	20011012 (9)
RELATED APPLN. INFO.:	Continuation-in-	part of	Ser. No. US 2001-818683,
	filed on 28 Mar	2001, PE	ENDING Continuation of
	Ser. No. US 1999	-305736,	filed on 5 May 1999,
	PENDING Continuat	tion-in-	-part of Ser. No. WO

NUMBER

			NUMBER	DATE	
PRIORITY	INFORMATION:	US	2000-239893P	20001013	(60)
		US	1997-64911P	19971107	(60)
		US	1997-64912P	19971107	(60)

US 1997-64983P 19971107 (60)
US 1997-64988P 19971107 (60)
US 1997-64988P 19971107 (60)
US 1997-64988P 19971107 (60)
US 1997-64988P 19971107 (60)
US 1997-64984P 19971107 (60)
US 1997-66094P 19971107 (60)
US 1997-660094P 19971117 (60)
US 1997-66095P 19971117 (60)
US 1997-66090P 19971117 (60)
US 1997-66090P 19971117 (60)
US 1997-66090P 19971117 (60)
Utility

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE,

ROCKVILLE, MD, 20850

NUMBER OF CLAIMS: 23 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 3 Drawing Page(s)

LINE COUNT: 36277

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating diseases, disorders, and/or conditions related to these novel human secreted proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCL INCLM: 536/023.200

INCLS: 435/069.100; 435/325.000; 435/320.100; 435/183.000

NCL NCLM: 536/023.200

NCLS: 435/069.100; 435/325.000; 435/320.100; 435/183.000

L67 ANSWER 5 OF 6 USPATFULL on STN

ACCESSION NUMBER: 2002:198286 USPATFULL

TITLE: rSOWgp58 protein and its use as an antigen INVENTOR(S): Hung, Chiung-Yu, Toledo, OH, UNITED STATES Cole, Garry T., Toledo, OH, UNITED STATES Medical College of Object (U.S. corporation)

PATENT ASSIGNEE(S): Medical College of Ohio (U.S. corporation)

NUMBER DATE

PRIORITY INFORMATION: US 2000-202754P 20000508 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: EMCH, SCHAFFER, SCHAUB & PORCELLO CO, P O BOX

916, ONE SEAGATE SUITE 1980, TOLEDO, OH, 43697

NUMBER OF CLAIMS: 32 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 6 Drawing Page(s)

LINE COUNT: 1476

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

The present invention provides bacterial plasymids and recombinant SOW proteins that are useful as antigens for serodiagnosis of

coccidiomycosis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCLM: 424/191.100

INCLS: 435/007.220; 530/395.000

NCLM: 424/191.100 NCL

NCLS: 435/007.220; 530/395.000

L67 ANSWER 6 OF 6 USPATFULL on STN

ACCESSION NUMBER: 2001:208993 USPATFULL

TITLE: Candida albicans gene (CSA1) encoding a mycelial

surface antigen, and uses thereof

INVENTOR(S): Bourbonnais, Yves, Cap-Rouge, Canada

Deslauriers, Noella, St-Ferreol-les-Neiges,

Canada

PATENT ASSIGNEE(S): Universite Laval, Quebec, Canada (non-U.S.

corporation)

NUMBER KIND DATE PATENT INFORMATION: US 6320033 B1 20011120 APPLICATION INFO.: US 1999-351200 19990709 19990709 (9)

NUMBER DATE

PRIORITY INFORMATION: CA 1998-2237134 19980710

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Marschel, Ardin H. LEGAL REPRESENTATIVE: Nixon Peabody LLP

NUMBER OF CLAIMS: EXEMPLARY CLAIM:

19 Drawing Figure(s); 11 Drawing Page(s) NUMBER OF DRAWINGS:

LINE COUNT: 810

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

The present invention relates to a Candida albicans gene (CSA1) AR encoding a surface protein. The present invention also relates to the surface protein and methods for using the protein or the gene for the detection, prophylaxis or treatment of candidal infection. The protein encoded is a surface antigen of Candida albicans yeast and mycelial forms, respectively. The mycelial surface antigen was shown to be present predominantly in the terminal third of the hyphal structures. CSAl is a gene coding for a unique surface antigen.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

INCLM: 536/023.100 INCL

INCLS: 435/006.000; 435/254.220; 536/023.740; 536/024.320

NCLM: 536/023.100 NCL

NCLS: 435/006.000; 435/254.220; 536/023.740; 536/024.320

(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, USPATFULL' ENTERED AT 09:47:30 ON 04 DEC 2003) L68 10292 S "COX R"?/AU

-Authoris L69 1193 S "MAGEE D"?/AU L70 5719 S "JIANG C"?/AU L71 21 S L68 AND L69 AND L70 L72 97 S L68 AND (L69 OR L70) L73 21 S L69 AND L70 L75 93 SEA ABB=ON PLU=ON (L71 OR L72 OR L73 OR L68 OR L69 OR L70) AND (L53 OR L30) L76 25 DUP REM L75 (68 DUPLICATES REMOVED) L76 ANSWER 1 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 1 ACCESSION NUMBER: 2003:790176 HCAPLUS TITLE: Identification of a protective antigen of Coccidioides immitis by expression library immunization Ivey, F. Douglas; Magee, D. Mitchell; AUTHOR(S): Woitaske, Melanie D.; Johnston, Stephen Albert; Cox. Rebecca A. CORPORATE SOURCE: Department of Microbiology and Immunology, University of Texas Health Science Center at San Antonio, San Antonio, TX, 78229, USA SOURCE: Vaccine (2003), 21(27-30), 4359-4367 CODEN: VACCDE; ISSN: 0264-410X Elsevier Science Ltd. PUBLISHER: Journal DOCUMENT TYPE: LANGUAGE: English Coccidioides immitis is a fungal pathogen of humans and is classified as a Select Agent. We have identified a new potential vaccine candidate for this pathogen using cDNA expression library immunization (ELI). A C. immitis spherule-phase cDNA library containing 800-1000 genes was divided into 10 pools and each was tested for its protective capacity in BALB/c mice against i.p. challenge with 2500 arthroconidia of this dimorphic fungus. The most protective pool, designated Pool 7, was fractionated into five sublibraries, each containing 60 genes, and of these, only Pool 7-3 induced a significant level of protection in mice. Fractionation of Pool 7-3 into six sublibraries, each with 10 genes, yielded a protective fraction, designated Pool 7-3-5. Subsequent fraction of the latter pool into 10 sublibraries, each with one clone, yielded a clone designated 7-3-5-5 that was highly protective. Clone 7-3-5-5 was sequenced and found to contain a 672 bp ORF encoding a 224 amino acid protein having a 19 amino acid signal sequence on the N-terminus and a 15 amino acid C-terminal GPI anchor site. 7-3-5-5 clone, designated ELI-Antigen 1 (ELI-Ag1), showed partial homol. with a hypothetical protein from Neurospora crassa. This is the first study to identify a protective antigen from a fungus using ELI, and it is also the first report in which sequential fractionation of an expression library successfully identified a single protective gene. L76 ANSWER 2 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 2 2003:721561 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 139:346526 TITLE: Transfection of murine dendritic cell line (JAWS II) by a nonviral transfection reagent

Searcher: Shears 308-4994

AUTHOR(S):

CORPORATE SOURCE:

Awasthi, Shanjana; Cox, Rebecca A.

Dept. of Pathology, University of Texas Health

Science Center at San Antonio, San Antonio, TX,

USA

SOURCE: BioTechniques (2003), 35(3), 600-602,604

CODEN: BTNQDO; ISSN: 0736-6205

PUBLISHER: Eaton Publishing Co.

DOCUMENT TYPE:

Journal

LANGUAGE: Enalish AB Dendritic cells are the most potent antigen-presenting cells that

initiate and modulate the host immune system. Based on their immunostimulatory activity, a variety of strategies have been developed to use dendritic cells as vaccines and immunotherapeutic agents against infection and cancer. Genetically modified dendritic cells are useful for immunotherapeutic purposes because of their sustained activity in vivo. However, transfection of dendritic cells with plasmid DNA has been very difficult. While the viral transfection is associated with nonspecific activation of dendritic cells, commonly used nonviral transfection reagents have a low efficiency of transfection. Here we describe an improved, simple, less time-consuming transfection protocol using the nonviral nonliposomal lipid polymer, TransIT-TKO transfection reagent, for transfecting murine dendritic cells (JAWS II) with the gene that encodes Coccidioides immitis antigen 2 (Ag2). The JAWS II cells were cotransfected with pHYG-enhanced green fluorescent protein (EGFP) and pVR1012-C immitis Ag2 plasmid DNAs using TransIT-TKO reagent. We reproducibly obtained

30%-50% transfection efficiency. The transfected cells maintained their immature phenotype and were functionally active. In addition, the flexibility of this agent for expressing multiple antigens (GFP and C. immitis Ag2) offers an advantage of

delivering multiple immunogens.

REFERENCE COUNT:

14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 3 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3

ACCESSION NUMBER:

2002:489694 HCAPLUS

DOCUMENT NUMBER:

137:92359

TITLE:

Role of signal sequence in vaccine-induced

protection against experimental

coccidioidomycosis

AUTHOR(S):

Jiang, Chengyong; Magee, D.

Mitchell; Ivey, F. Douglas; Cox,

Rebecca A.

CORPORATE SOURCE:

Department of Microbiology, University of Texas

Health Science Center at San Antonio, San

Antonio, TX, 78229, USA

SOURCE:

Infection and Immunity (2002), 70(7), 3539-3545

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: DOCUMENT TYPE: American Society for Microbiology

Journal English LANGUAGE:

The vaccine efficacy of the gene sequence encoding the signal peptide of the antigen known as antigen 2 or proline-rich antigen (Ag2/PRA), an immunodominant antigen present in the cell wall of the fungal pathogen Coccidioides immitis, was investigated in a murine model of coccidioidomycosis. Expression plasmids for Ag2/PRA(1-18) DNA (signal sequence), Ag2/PRA(19-194) DNA (lacking the signal sequence), and

Ag2/PRA(1-194) DNA (full length) were inserted in the pVR1012 vector, and the constructs were used to vaccinate the highly susceptible BALB/c mouse strain. Immunization with the signal gene sequence significantly reduced the fungal burden in the lungs and spleens of mice 12 days after i.p. challenge with a LD of 2500 C. immitis arthroconidia, to a level comparable to the protection induced in mice immunized with the full-length Ag2/PRA(1-194) DNA. The Ag2/PRA(19-194) gene protected mice but to a significantly lower level than the signal sequence or the full-length Ag2 gene. The immunizing capacity of Ag2/PRA(1-18) was not attributable to a nonspecific immunostimulatory effect of DNA, as evidenced by the fact that mice immunized with a frameshift mutation of Ag2/PRA(1-18) were not protected against challenge. Furthermore, a synthetic peptide corresponding to the translated sequence of Ag2/PRA(1-18) DNA protected mice, albeit at a lower level than the Ag2/PRA(1-18) DNA vaccine. The protection induced with the signal gene vaccine correlated with the production of gamma interferon when splenocytes from Ag2/PRA(1-18)-immunized mice were stimulated with recombinant full-length Ag2 and was not associated with the production of anti-Coccidioides IgG antibody. is the first study to establish that a signal peptide sequence alone, administered as a gene vaccine or synthetic peptide, can induce protective immunity against a microbial pathogen.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L76 ANSWER 4 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on

STN

ACCESSION NUMBER: 2002:597076 BIOSIS DOCUMENT NUMBER: PREV200200597076

TITLE: Induction of gene expression in **Coccidioides** immitis during growth inside murine macrophages.

AUTHOR(S): Magee, D. M. [Reprint author]; Woitaske, M.

D. [Reprint author]; Wickes, B. L. [Reprint author];

Cox, R. A. [Reprint author]

CORPORATE SOURCE: University of Texas Health Science Center at San

Antonio, San Antonio, TX, USA

SOURCE: Abstracts of the General Meeting of the American

Society for Microbiology, (2002) Vol. 102, pp. 205.

print.

Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.

ISSN: 1060-2011.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 20 Nov 2002

Last Updated on STN: 20 Nov 2002

AB Coccidioides immitis is a dimorphic fungus of the American southwest growing in the soil as mycelia and within the host as the spherule/endospore parasitic phase. We hypothesized that genes that are upregulated when C. immitis grows in vivo might be associated with virulence of this primary fungal pathogen. To identify potential virulence-associated genes, we utilized differential display, reverse transcriptase, polymerase chain

reaction (DD-RT-PCR) to assess induction of gene expression within C. immitis spherules during intracellular parasitism of murine macrophages. Macrophage monolayers were infected with C. immitis arthroconidia and, after approximately 36 hours of culture, RNA was obtained from the developing macrophage-derived spherules and compared to RNA from spherules grown in tissue culture medium alone. Differential display analyses identified 11 gene fragments specific for the macrophage-derived spherules. These products were cloned into a TA vector, sequenced, and analyzed for homology with the Genbank databases. One clone had significant homology to a Magnaporthe grisea appressorium stage cDNA library gene and Saccharomyces cerevisae glycogen phosphorylase. The complete cDNA clone was recovered using 5' and 3' RACE and using this as a probe, we obtained and sequenced a genomic clone for C. immitis glycogen phosphorylase. The gene had seven predicted introns and a translation of the coding region indicated that the protein would contain 881 amino acids with a molecular weight of 100.6 kDa and a pI of 5.75. Northern analysis confirmed that glycogen phosphorylase message was differentially expressed by spherules in parasitized macrophages. Differential display may provide a tool to delineate virulence-associated genes of C. immitis or help define metabolic targets for rationally designed antifungal drugs.

L76 ANSWER 5 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 4

2000:208899 HCAPLUS ACCESSION NUMBER:

132:247984 DOCUMENT NUMBER:

The x-ray structure of a chitinase from the TITLE:

pathogenic fungus Coccidioides immitis

Hollis, Thomas; Monzingo, Arthur F.; Bortone, AUTHOR(S):

Kara; Ernst, Stephen; Cox, Rebecca;

Robertus, Jon D.

Institute of Cellular and Molecular Biology, CORPORATE SOURCE:

Department of Chemistry and Biochemistry, University of Texas, Austin, TX, 78712, USA

Protein Science (2000), 9(3), 544-551 SOURCE:

CODEN: PRCIEI; ISSN: 0961-8368

Cambridge University Press PUBLISHER:

DOCUMENT TYPE: Journal

LANGUAGE: English

The x-ray crystal structure of chitinase from C. immitis was solved to 2.2 Å resolution Like other members

of the class 18 hydrolase family, this 427-residue protein was an 8-stranded β/α -barrel. Although lacking an N-terminal chitin-anchoring domain, the enzyme closely resembled

chitinase from Serratia marcescens. Among the conserved features were 3 cis peptide bonds, all involving conserved active

site residues. The active site was formed from conserved residues

such as Trp-47, Trp-131, Trp-315, Trp-378, Tyr-239, Tyr-293, Arg-52 and Arg-295. Glu-171 was the catalytic acid in the hydrolytic mechanism; when it was mutated to Gln, enzyme activity was abolished. Allosamidin is a substrate analog that strongly inhibits

the class 18 enzymes. Its binding to the chitinase, hevamine, was previously observed and conserved structural features of the 2 enzymes were used to predict the inhibitor's binding to the fungal enzyme.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L76 ANSWER 6 OF 25 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS

RESERVED. on STN

CORPORATE SOURCE:

ACCESSION NUMBER: 1999185649 EMBASE

TITLE: Construction of a single-chain interleukin-12-

expressing retroviral vector and its application in

cytokine gene therapy against experimental

coccidioidomycosis.

AUTHOR: Jiang C.; Magee D.M.; Cox

R.A.

C. Jiang, Dept. of Clinical Investigation, Texas Center for Infectious Disease, 2303 SE Military Dr.,

San Antonio, TX 78223, United States.

chengyong.jiang@tdh.state.tx.us

Infection and Immunity, (1999) 67/6 (2996-3001). SOURCE:

Refs: 45

ISSN: 0019-9567 CODEN: INFIBR

COUNTRY: United States DOCUMENT TYPE: Journal; Article FILE SEGMENT: 004 Microbiology

> 026 Immunology, Serology and Transplantation

LANGUAGE: English SUMMARY LANGUAGE: English

T-cell-mediated immunity is an important determinant in protection

against primary infection with Coccidioides immitis, a dimorphic fungal pathogen that causes the disease

coccidioidomycosis. To determine if interleukin-12 (IL-12) gene therapy could potentiate host response against C.

immitis, we constructed a single-chain cDNA encoding the p40 and p35 subunits linked by a polylinker and, using a retroviral vector, transfected J774 macrophages with the construct. The transduced J774 cells expressed IL-12 in vitro, with a mean concentration of 28,440 pg from 106 cells in 48 h as measured by an

IL-12 (p75)-specific enzyme-linked immunosorbent assay. The secreted IL-12 was biologically active, as judged by its ability to induce the production of gamma interferon (IFN- γ) by spleen cells

from BALB/c mice. Treatment of the highly susceptible BALB/c mouse strain with the IL-12- transduced J774 cells inhibited C.

immitis growth in tissues from mice challenged by a pulmonary route, as evidenced by 1.37-, 2.59-, and 1.22-log

reductions in the number of CFU in the lungs, spleens, and livers,

respectively, compared to the fungal load in mice given

vector-transduced J774 cells. The protective effect of IL-12 gene therapy was accompanied by increased levels of IFN- γ in the

lungs and sera of mice treated with IL-12- transduced J774 cells and

the constitutive production of IFN- γ by their spleen cells cultured in vitro. These results suggest that IL-12 gene therapy

could be used as adjunct therapy for coccidioidomycosis.

L76 ANSWER 7 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 5 ACCESSION NUMBER: 1999:83280 HCAPLUS

DOCUMENT NUMBER: 130:266091

TITLE: Genetic vaccination against Coccidioides

immitis: comparison of vaccine efficacy of recombinant antigen 2 and antigen 2 cDNA

AUTHOR(S): Jiang, Chengyong; Magee, D.

Mitchell; Quitugua, Teresa N.; Cox,

Rebecca A.

CORPORATE SOURCE: Department of Clinical Investigation, Texas

Center for Infectious Disease, San Antonio, TX,

78223, USA

SOURCE: Infection and Immunity (1999), 67(2), 630-635

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

AB Previous studies from our laboratory established that C-ASWS, an alkali-soluble, water-soluble extract from cell walls of **Coccidioides** immitis, protects mice against lethal challenge with this fungus.

The C-ASWS extract contains a glycosylated protein,

designated antigen 2 (Ag2), and a polysaccharide antigen. We recently cloned Ag2 cDNA and showed that the recombinant fusion

protein elicited strong delayed-type hypersensitivity

responses in immunized mice. This investigation was undertaken to determine if the recombinant Ag2 protein, expressed as an

Ag2-glutathione S-transferase (GST) fusion **protein**, or Ag2 cDNA would protect mice against lethal challenge with **C**.

immitis. The recombinant Ag2-GST protein

protected BALB/c mice against i.p. challenge with 250 arthroconidia,

as assessed by a decrease in fungal CFU in tissues. The

Ag2-GST-immunized mice did not show, however, an increased survival during a 30-day period postinfection. By contrast, immunization of mice with Ag2 cDNA ligated into the pVR1012 plasmid engendered protection against i.p. challenge with 2,500 arthroconidia and against pulmonary challenge with 50 arthroconidia. Vaccine efficacy

against pulmonary challenge with 50 arthroconidia. Vaccine efficacy

paralleled the development of delayed-type hypersensitivity

responses to C. immitis antigen. Whereas mice

vaccinated with the recombinant Ag2-GST protein did not

mount footpad hypersensitivity to C-ASWS or the recombinant Ag2-GST

protein, mice vaccinated with the pVR1012-Ag2 construct

mounted a strong footpad hypersensitivity and their spleen cells

secreted gamma interferon upon in vitro stimulation with the

Ag2-containing C-ASWS extract This is the first investigation to show that

genetic immunization can protect against lethal challenge with

C. immitis.

SOURCE:

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L76 ANSWER 8 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 6

ACCESSION NUMBER: 1999:2211 HCAPLUS

DOCUMENT NUMBER: 130:135866

TITLE: Crystallization and preliminary x-ray analysis

of a chitinase from the fungal pathogen

Coccidioides immitis

AUTHOR(S): Hollis, Thomas; Monzingo, Arthur F.; Bortone,

Kara; Schelp, Elisabeth; Cox, Rebecca;

Robertus, Jon D.

CORPORATE SOURCE: Institute of Cellular and Molecular Biology,

Department of Chemistry and Biochemistry, University of Texas, Austin, TX, 78712, USA Acta Crystallographica, Section D: Biological

Crystallography (1998), D54(6, Pt. 2), 1412-1413

CODEN: ABCRE6; ISSN: 0907-4449
PUBLISHER: Munksgaard International Publishers Ltd.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Chitinase from C. immitis was expressed as a fusion protein with gluathione-S-transferase (GST), which aided in its purification After cleavage from GST, the chitinase was crystallized from 30% PEG 4000 in 0.1M NaOAc, pH 4.6. The crystals had a tetragonal crystal lattice and belonged to space group P41212 or P43212 and diffracted to 2.2 Å resolution The unit-cell parameters were a = b = 91.2, c = 95.4 Å; there is only 1 chitinase mol. in the asym. unit.

REFERENCE COUNT:

12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L76 ANSWER 9 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 7

ACCESSION NUMBER:

1997:655696 HCAPLUS

DOCUMENT NUMBER:

127:330024

TITLE:

Mapping of a Coccidioides

immitis-specific epitope that reacts with

complement-fixing antibody

AUTHOR(S):

Yang, Michael C.; Magee, D. Mitchell;

Cox, Rebecca A.

CORPORATE SOURCE:

Department of Clinical Investigation, Texas

Center for Infectious Disease, San Antonio, TX,

78223, USA

SOURCE:

Infection and Immunity (1997), 65(10), 4068-4074

CODEN: INFIBR; ISSN: 0019-9567 American Society for Microbiology

PUBLISHER: DOCUMENT TYPE: Journal

LANGUAGE: English

The authors have previously cloned the cDNA fragment that encodes the complement fixation antigen of Coccidioides immitis. The recombinant protein was highly sensitive in detecting CF antibody in sera from patients with coccidioidomycosis but was not specific to C. immitis, as evidence by its reactivity with sera from patients with histoplasmosis and, to lesser extent, blastomycosis. The authors undertook this study to determine if the epitope(s) that reacts with CF antibody is the same

or differs from the epitopes that are shared with Histoplasma capsulatum and Blastomyces dermatitidis. PCR-generated CF/chitinase cDNA fragments were cloned and examined for their reactivity in enzyme-linked immunosorbent assays using sera from patients with coccidioidomycosis, histoplasmosis, or blastomycosis. A peptide domain comprised of amino acid residues 20 through

310 was shown to express an epitope(s) that is specific to anti-Coccidioides CF antibody. The peptide detected serum antibody in 21 (95%) of 22 patients with active coccidioidomycosis and was without reactivity with sera from

20 patients with histoplasmosis, 15 patients with blastomycosis, and 14 healthy subjects. Antibody titers to the recombinant peptide directly correlated with CF antibody titers (P <

0.01), and preadsorption of reference CF antiserum with the peptide ablated the reactivity of the antiserum in the immunodiffusion assay for CF antibody. The delineation of a recombinant peptide that has both sensitivity and

specificity will provide a valuable tool for detecting CF antibody and for evaluating the role of CF antibody in the host response to

C. immitis.

L76 ANSWER 10 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 8

ACCESSION NUMBER:

1997:482804 HCAPLUS

DOCUMENT NUMBER:

127:204149

Identification of a Coccidioides

immitis antigen 2 domain that expresses

B-cell-reactive epitopes

AUTHOR(S):

Zhu, Yufan; Tryon, Vic; Magee, D.

Mitchell; Cox, Rebecca A.

CORPORATE SOURCE:

Department of Clinical Investigation, Texas Center for Infectious Disease, San Antonio, TX,

78223, USA

SOURCE:

Infection and Immunity (1997), 65(8), 3376-3380

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER:

American Society for Microbiology

DOCUMENT TYPE:

Journal

LANGUAGE:

English Antigen 2 (Ag2), a major immunoreactive component of C. immitis mycelium- and spherule-phase cell walls, was

recently cloned and was shown to elicit T-cell responses in

Coccidioides-immune mice. Here, the authors evaluated recombinant Ag2 (rAg2) and PCR-generated Ag2 truncations for expression of B-cell-reactive epitopes in ELISA and immunoblot

assays with sera from patients with active

coccidioidomycosis, a hyperimmune goat anti-Ag2 serum, and a murine anti-Ag2 monoclonal antibody that recognizes a conformational epitope. The results established that rAg2 expresses both linear and conformational B-cell-reactive epitopes which are localized to a

domain comprised of amino acids 19-96 (designated A19-96). Truncations designed to identify epitopes within the A19-96 domain yielded fragments that either were nonreactive (A62-194, A19-61, and

A49-79) or showed reduced reactivity (A19-79). Hence, A19-96 was the shortest domain expressing epitopes recognized by the panel of antibodies. The prevalence of antibodies to the A19-96 domain was

evaluated in ELISAs of sera from 28 coccidioidomycosis

patients. Antibody reactivity was detected in 79% of the patients' sera, and the level of antibody reactivity was directly correlated with disease severity. Whereas patients with pulmonary disease showed a mean response (A405) of 0.16, patients with disseminated

coccidioidomycosis showed a mean response of 0.69. No reactivity was detected with sera from histoplasmosis or

blastomycosis patients. The production of a recombinant peptide that expresses C. immitis-specific Ag2 epitopes

provides a useful reagent for examining the role of anti-Ag2 antibodies in coccidioidomycosis.

DUPLICATE 9 L76 ANSWER 11 OF 25 MEDLINE on STN

ACCESSION NUMBER:

97160980 MEDLINE

DOCUMENT NUMBER: TITLE:

97160980 PubMed ID: 9008276 Recombinant Coccidioides immitis

complement-fixing antigen: detection of an epitope

shared by C. immitis, Histoplasma

capsulatum, and Blastomyces dermatitidis. Yang M C; Magee D M; Kaufman L; Zhu Y;

CORPORATE SOURCE:

AUTHOR:

Department of Clinical Investigation, Texas Center for Infectious Disease, San Antonio 78223, USA.

CONTRACT NUMBER: AI12431 (NIAID)

SOURCE: CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, (1997

Jan) 4 (1) 19-22.

Journal code: 9421292. ISSN: 1071-412X.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199704

ENTRY DATE: Entered STN: 19970422

Last Updated on STN: 19970422 Entered Medline: 19970408

AB We undertook an investigation to assess the utility of a recombinant

Coccidioides immitis complement-fixing (CF) antigen for

detecting CF antibody in sera from patients with coccidioidomycosis. Enzyme-linked immunosorbent assays established that recombinant CF antigen and, for comparison, a commercially available coccidioidin were reactive with 19 of 19 sera from patients with active coccidioidomycosis. The recombinant antigen was significantly more sensitive than coccidioidin. The median titer obtained when patients' sera were assayed against recombinant CF antigen was 1:51,200 compared to 1:25,600 with coccidioidin (P < 0.027). The recombinant antigen was also more effective in distinguishing the antibody levels in sera from patients with pulmonary coccidioidomycosis than in sera from those with disseminated disease. Whereas patients with pulmonary disease showed a median antibody titer of 1:25,600, those with multifocal disease showed a median titer of 1:102,400 (P < 0.028). The recombinant CF antigen was found, however, to express an epitope(s) that reacted with sera from 6 of 12 patients with histoplasmosis and 2 of 12 patients with

L76 ANSWER 12 OF 25 MEDLINE on STN ACCESSION NUMBER: 96355868 MEDLINE

DOCUMENT NUMBER: 96355868 PubMed ID: 8751906

TITLE: Interleukin-12 regulation of host defenses against

Coccidioides immitis.

AUTHOR: Magee D M; Cox R A

CORPORATE SOURCE: Department of Clinical Investigation, Texas Center

for Infectious Diseases, San Antonio 78223, USA...

mmagee@tcid.tdh.state.tx.us

CONTRACT NUMBER: AI23555 (NIAID)

SOURCE: INFECTION AND IMMUNITY, (1996 Sep) 64 (9) 3609-13.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

blastomycosis.

FILE SEGMENT: Priority Journals; AIDS

ENTRY MONTH: 199610

ENTRY DATE: Entered STN: 19961015

Last Updated on STN: 19961015 Entered Medline: 19961003

AB We have previously reported on the alternate regulation of gamma interferon (IFN-gamma) and interleukin-4 (IL-4) in inbred mouse strains which differ in their susceptibility to **Coccidioides** immitis. The genetically resistant DBA/2 mice manifest a predominant T-helper 1 (Th1) response, with early production of IFN-gamma, whereas susceptible BALB/c mice show an early production

of the Th2 cytokine IL-4. Since IL-12 is one cytokine that can act early during host defenses to promote the differentiation of cytokine production towards IFN-gamma and thus may promote expression of a protective immune response, we investigated the role of IL-12 in resistance to C. immitis. Administration of recombinant IL-12 to the susceptible mouse strain before and after systemic (intraperitoneal) challenge with C . immitis significantly ameliorated the course of the disease, as measured by a reduction in the fungal load in the lungs, liver, and spleen. Analysis of the cytokine mRNA in lungs from infected BALB/c mice revealed that the protective effect of recombinant IL-12 was accompanied by a shift from a Th2 to a Th1 response. The importance of IL-12 in resistance to this fungus was further established by showing that neutralization of endogenous IL-12 in the resistant DBA/2 mouse strain led to a significant increase in the fungal burden in pulmonary and extrapulmonary tissues. These results establish that IL-12 plays a pivotal role in the host defense against systemic challenge with C. immitis.

L76 ANSWER 13 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 10

ACCESSION NUMBER: 1996:391996 HCAPLUS

DOCUMENT NUMBER: 125:55750

TITLE: Molecular cloning and characterization of

Coccidioides immitis antigen 2 cDNA

AUTHOR(S): Zhu, Yufan; Yang, Chunmu; Magee, D.

Mitchell; Cox, Rebecca A.

CORPORATE SOURCE: Dep. Clinical Investigation, Texas Center

Infectious Disease, San Antonio, TX, 78223, USA Infection and Immunity (1996), 64(7), 2695-2699

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

SOURCE:

Previous expts. have provided evidence that Coccidioides immitis antigen 2 (Ag2) is a major T-cell-reactive component of mycelia and spherule cell walls. Here the authors report the identification and cloning of the cDNA that encodes Ag2 from a lambda ZAP cDNA expression library constructed from spherule-derived RNA. DNA sequence anal. established that the 1,255-bp clone contains a 174-bp 5' untranslated region, a 582-bp open reading frame which encodes for a protein consisting of 194 amino acids, and a 375-bp 3' untranslated region, including a poly(A) tail. The recombinant Ag2 protein has a predicted mol. mass of 19.5 kDa and contains an 18-amino-acid N terminus which has been tentatively identified as a signal peptide. The Ag2 cDNA was ligated into the pGEX-4T-3 vector and expressed in Escherichia coli TG-1 cells as a glutathione S-transferase fusion protein. The recombinant fusion protein showed reactivity with sera from patients with coccidioidomycosis and elicited delayed-type footpad hypersensitivity responses in Coccidioides-immune mice. These results suggest that the Ag2 cDNA can be used for the large-scale production of this immunol. important protein.

L76 ANSWER 14 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 11

ACCESSION NUMBER: 1996:327965 HCAPLUS

DOCUMENT NUMBER: 125:28509

TITLE: Molecular cloning and characterization of the

Coccidioides immitis complement

fixation/chitinase antigen

AUTHOR(S): Yang, Chunmu; Zhu, Yufan; Magee, D.

Mitchell; Cox, Rebecca A.

CORPORATE SOURCE: Department Clinical Investigation, Texas Center

Infectious disease, San Antonio, TX, 78223, USA Infection and Immunity (1996), 64(6), 1992-1997

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

Journal DOCUMENT TYPE: LANGUAGE: English

SOURCE:

Detection of anti-Coccidioides complement-fixing (CF) antibody is a valuable diagnostic and prognostic aid in coccidioidomycosis. The CF antibody response is directed

against a heat-labile antigen that has chitinase activity, hereafter referred to as the CF/chitinase protein. To identify and

clone this immunoreactive enzyme, the authors constructed a Coccidioides immitis cDNA lambda ZAP expression library from

spherule RNA and detected fusion peptides expressing CF

epitopes by immunoscreening. A cDNA clone consisting of 1623 bp was identified, sequenced, and found to contain a single open reading

frame that encodes a protein of 47 kDa with 427 amino

acids. Deduced amino acid sequence analyses showed that the cloned CF/chitinase cDNA contains a 35-amino-acid region, beginning at Ser-18 and ending at Arg-52, which has 92% homol. with the reported

N-terminal amino acid sequence of authentic CF/chitinase protein. The first 17 amino acids in the deduced sequence of the cloned cDNA are not present on the mature CF/chitinase protein, suggesting that it may be a signal peptide

Expression of the CF/chitinase cDNA insert by using the pGEX-4T-3 vector yields a fusion peptide that bears CF-specific epitopes and shows chitinase activity. The CF/chitinase clone will enable large-scale production of the recombinant CF antigen for use in immunoassays and facilitate studies on the role of chitinase in the

morphogenesis of C immitis.

L76 ANSWER 15 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 12

ACCESSION NUMBER: 1996:737195 HCAPLUS

DOCUMENT NUMBER: 126:86206

TITLE: Coccidioides immitis Antigen 2: analysis of gene and protein

Zhu, Yufan; Yang, Chunmu; Magee, D. AUTHOR(S):

Mitchell; Cox, Rebecca A.

Department of Clinical Investigation, Texas CORPORATE SOURCE:

Center for Infectious Disease, 2303 SE Military

Drive, San Antonio, TX, 78223, USA

Gene (1996), 181(1/2), 121-125

CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier DOCUMENT TYPE: Journal

LANGUAGE: English

SOURCE:

Antigen 2 is a glycosylated protein present in the cell walls of the dimorphic fungus Coccidioides immitis. Using

oligodeoxyribonucleotide (oligo) primers based on the sequences of Ag2 cDNA, the gene encoding Ag2 was cloned from genomic DNA derived from the mycelial phase of C. immitis by PCR.

Nucleotide (nt) sequence analyses showed a 582 base pair (bp) ORF

disrupted by two introns which are 78bp and 10lbp long. The deduced primary translation product consists of 194 amino acids (aa), contains an N-terminal putative signal sequence to allow transport into the endoplasmic reticulum, and a C-terminal putative signal sequence to enable a GPI anchor addition Putative GPI anchor/cleavage site and O-glycosylation sites, as well as phosphorylation and myristoylation sites are also present. On the basis of these analyses, the authors predict that a prepro-Ag2 undergoes a post-translational modification to yield the mature glycosylated Ag2 protein which is anchored on the extracellular plasma membrane of mycelial and spherule-phase cells.

L76 ANSWER 16 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 13

ACCESSION NUMBER: 1995:781432 HCAPLUS

DOCUMENT NUMBER: 123:196430

TITLE: Roles of gamma interferon and interleukin-4 in

genetically determined resistance to

Coccidioides immitis

AUTHOR(S): Magee, D. Mitchell; Cox, Rebecca

Δ

CORPORATE SOURCE: Dep. Res. Immunol., Texas Cent. Infectious

Diseases, San Antonio, TX, 78223, USA

SOURCE: Infection and Immunity (1995), 63(9), 3514-19

CODEN: INFIBR; ISSN: 0019-9567

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

AB The profiles of γ interferon (IFN-γ) and interleukin-4 (IL-4) production were valuated during the course of coccidioidomycosis in 2 inbred mouse strains which differ in their susceptibility to C. immitis. Cytokine responses, measured at the mol. and protein levels, showed increased levels of IFN-γ in lung exts. from mice of the resistant DBA/2 strain after a pulmonary challenge, whereas the susceptible BALB/c strain manifested a predominant IL-4 response. The importance of these cytokines in host defense against C. immitis was established by treating the mice with recombinant cytokines or neutralizing anticytokine monoclonal antibodies. Treatment of the susceptible BALB/c mice with recombinant murine IFN-γ protected mice against systemic

recombinant murine IFN- γ protected mice against systemic challenge, and in the reciprocal experiment, the administration of an anti-IFN- γ monoclonal antibody to the resistant DBA/2 mice decreased their capacity to control disease. Although the treatment of DBA/2 mice with recombinant IL-4 did not alter the disease, neutralization of endogenous IL-4 in infected BALB/c mice by administration of a neutralizing anti-IL-4 antibody led to a reduction in the fungal load in their tissues. Apparently, IFN- γ plays a pivotal role in resistance to **C. immitis**, whereas IL-4 down-regulates protective immunity against **C**.

whereas 1L-4 down-regulates protective immunity against C immitis.

L76 ANSWER 17 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 14

ACCESSION NUMBER: 1993:426295 HCAPLUS

DOCUMENT NUMBER: 119:26295

TITLE: Production of a murine monoclonal antibody that

recognizes an epitope specific to Coccidioides immitis antigen 2

AUTHOR(S): Cox, Rebecca A.; Dolan, Matthew J.;

Magee, D. Mitchell; Galgiani, John N.

CORPORATE SOURCE: Dep. Res. Immunol., San Antonio State Chest

Hosp., San Antionio, TX, 78223, USA

SOURCE: Infection and Immunity (1993), 61(5), 1895-9

CODEN: INFIBR; ISSN: 0019-9567

DOCUMENT TYPE: Journal LANGUAGE:

English

Antigen 2 (Ag2) has been implicated as a T-cell-reactive component

of the pathogenic fungus C. immitis. This

report describes the production of a murine monoclonal antibody (MAb) of

the IgG2a isotype that recognizes an epitope specific to C

.immitis Ag2. This specificity was evidenced by the

finding that the MAb did not recognize other antigens present in coccidioidin or spherulin and did not show reactivity with antigenic exts. from Histoplasma capsulatum or Blastomyces

dermatitidis. The epitope was labile to enzymic digestion with pronase but resistant to treatment with glycolytic enzymes and to periodate oxidation This peptide epitope appears to require conformational structure because it was not recognized by the MAb in

immunoblots of antigen that had been electrophoresed in polyacrylamide gels under denaturing, reducing conditions.

Immunoaffinity chromatog, of spherulin on columns containing the MAD established that the MAb was effective as a ligand for isolating Ag2 from heterogeneous exts. The production of a MAb which recognizes an Ag2-specific epitope and its utility as a ligand for isolating Ag2 will provide a valuable reagent for studies of this immunol.

important antigen.

L76 ANSWER 18 OF 25 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 15

ACCESSION NUMBER: 92245388 EMBASE

DOCUMENT NUMBER: 1992245388

TITLE: Localization of the tube precipitin and complement

fixation antigens of Coccidioides immitis

by immunoelectron microscopy with murine monoclonal

antibodies.

AUTHOR: Cox R.A.; Sun S.H.; Dolan M.J.; Harrison

J.L.

CORPORATE SOURCE: Department of Research Immunology, San Antonio State

Chest Hospital, San Antonio, TX 78223, United States

Infection and Immunity, (1992) 60/8 (3315-3324). ISSN: 0019-9567 CODEN: INFIBR SOURCE:

COUNTRY: United States

DOCUMENT TYPE: Journal; Article FILE SEGMENT: 004 Microbiology

005 General Pathology and Pathological Anatomy

026 Immunology, Serology and Transplantation

LANGUAGE: English SUMMARY LANGUAGE: English

The cellular localization of the tube precipitin (TP) and complement fixation (CF) antigens of Coccidioides immitis was examined by immunoelectron microscopy with murine immunoglobulin G1 monoclonal antibodies directed against the TP and CF antigens, respectively. Immunoelectron microscopic analyses of saprobic- and parasitic-phase cells showed that the TP antigen is present at a high concentration within the inner cell wall layer and along the plasma membrane. The antigen was also detected, at a lesser

concentration, within cytoplasmic vacuoles. In contrast to the

predominant localization of the TP antigen in the cell walls, the CF antigen resides primarily within the cytoplasm, where it appears to be dispersed throughout the cytoplasm rather than associated with a specific cytoplasmic organelle. A sparse amount of the CF antigen within the inner cell walls was also demonstrable. The localization of the TP and CF antigens throughout the morphogenetic phases of C. immitis has important implications in antigen production and in analyses of host response in coccidioidomycosis.

L76 ANSWER 19 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 16

1991:533582 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 115:133582

TITLE: An immunoreactive apoglycoprotein purified from

Coccidioides immitis

Dugger, Kris O.; Galgiani, John N.; Ampel, Neil AUTHOR(S):

M.; Sun, Sung H.; Magee, D. Mitchell;

Harrison, Jeff; Law, John H.

Med. Res. Serv., Veterans Aff. Med. Cent., CORPORATE SOURCE:

Tucson, AZ, 85723, USA

SOURCE: Infection and Immunity (1991), 59(7), 2245-51

CODEN: INFIBR; ISSN: 0019-9567

DOCUMENT TYPE: Journal . English LANGUAGE:

Deglycosylation of glycoproteins in a lysate of spherules of C. immitis has permitted purification and partial

characterization of a proline-rich pronase-sensitive antigen. Moreover, soluble antigen specifically stimulated lymphocytes from

persons with dermal delayed-type hypersensitivity to

coccidioidal antigens. When related to reference

coccidioidin by tandem 2-dimensional immunoelectrophoresis,

the antigen fused in the anodal region with a specific reference antigen

(antigen 2). It did not show identity with coccidioidal

antigens used in conventional serol. assays. Although immunoblots of the purified protein with monospecific rabbit antiserum showed a single antigen at 33 kDa, the parent spherule lysate bound the same antibody in a broad band between 70 and >200 kDa, which

could be explained by microheterogeneity of glycosylation.

Immunoelectron microscopy using affinity-purified human antibodies localized the antigen to the cell wall and internal septa of spherules. The apoglycoprotein may be important in human immune

responses to coccidioidal infection.

L76 ANSWER 20 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 17

1991:490408 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 115:90408

Production and characterization of a monoclonal TITLE:

antibody to the complement fixation antigen of

Coccidioides immitis

Dolan, Matthew J.; Cox, Rebecca A. AUTHOR(S):

Dep. Res. Immunol., San Antonio State Chest Hosp., San Antonio, TX, 78223, USA CORPORATE SOURCE:

Infection and Immunity (1991), 59(6), 2175-80 SOURCE:

CODEN: INFIBR; ISSN: 0019-9567

DOCUMENT TYPE: Journal LANGUAGE: English

AB · Detection of complement-fixing antibody to coccidioidin by

using the complement fixation test or an immunodiffusion assay for

complement-fixing antibody (IDCF) is widely viewed as the most useful immunodiagnostic test for coccidioidomycosis. Here is reported the production of an IgG1 monoclonal antibody (MAb) to the IDCF antigen for use as a biospecific ligand for purifying the IDCF antigen on solid-phase immunosorbents and for use as a reagent for screening genomic or cDNA expression libraries from C. immitis. BALB/c mice were immunized by i.m. injections of coccidioidin in adjuvant, followed by an intrasplenic booster injection of coccidioidin in saline. The spleen cells were fused with SP2/O Ag14 myeloma cells, and the fusion products were screened for IgG antibody to coccidioidin by using an ELISA. Pos. hybridomas were cloned and evaluated for reactivity to the IDCF antigen by 2-dimensional immunoelectrophoresis and by immunoblotting. The epitope recognized by the MAb was heat labile (60°, 30 min) and susceptible to enzymic digestion with pronase but was resistant to treatment with lipase, α -mannosidase, glucose oxidase, and endoglycosidase H. This heat-labile peptide epitope appears to be specific to C. immitis, as judged by the fact that the MAb was not reactive in immunoblots or ELISAs of histoplasmin or blastomycin.

L76 ANSWER 21 OF 25 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 18

ACCESSION NUMBER: 1989:455564 HCAPLUS

DOCUMENT NUMBER: 111:55564

AUTHOR(S):

TITLE: Induction of tumor necrosis factor alpha by

spherules of **Coccidioides** immitis Slagle, David C.; **Cox, Rebecca A**.;

Kuruganti, Uma

CORPORATE SOURCE: Dep. Res. Immunol., San Antonio State Chest

Hosp., San Antonio, TX, 78223, USA

SOURCE: Infection and Immunity (1989), 57(7), 1916-21

CODEN: INFIBR; ISSN: 0019-9567

DOCUMENT TYPE: Journal LANGUAGE: English

LANGUAGE: The cytokine tumor necrosis factor α (TNF- α) functions as an immunomodulatory protein and as a mediator of cachexia. Here, the viable or formalin-killed spherules of C. immitis induced the secretion of TNF- α by peritoneal-exudate cells from BALB/c mice. The identification of the cytokine as TNF- α was based on its lytic activity against the TNF- α -sensitive Ls murine fibrosarcoma cell line but not the TNF- α -resistant LR cell line, its neutralization by rabbit anti-TNF- α , and its secretion by peritoneal cells having characteristics of macrophages. The induction of TNF- α was attributable to spherules and not to contaminating lipopolysaccharide (endotoxin), as evidenced by the finding that polymyxin B, a reagent that blocks the TNF- α -inducing component of lipopolysaccharide, did not negate the production of $TNF-\alpha$ in response to spherules, whereas pretreatment of spherules with hyperimmune goat antiserum to spherulin neutralized the induction of TNF- α by these cells. The demonstration that C. immitis activates macrophages to secrete $TNF-\alpha$ in vitro is a new finding and warrants studies to determine whether this cytokine is produced during active coccidioidomycosis.

L76 ANSWER 22 OF 25 MEDLINE on STN DUPLICATE 19

ACCESSION NUMBER: 88085464 MEDLINE

DOCUMENT NUMBER: 88085464 PubMed ID: 3335400

TITLE: Induction and expression of cell-mediated immune

responses in inbred mice infected with

Coccidioides immitis.

AUTHOR: Cox R A; Kennell W; Boncyk L; Murphy J W

CORPORATE SOURCE: Department of Research Immunology, San Antonio State

Chest Hospital, Texas 78223.

CONTRACT NUMBER: AI23555 (NIAID)

SOURCE: INFECTION AND IMMUNITY, (1988 Jan) 56 (1) 13-7.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

198802 ENTRY MONTH:

ENTRY DATE: Entered STN: 19900305

Last Updated on STN: 19970203 Entered Medline: 19880209

Comparisons of the course of coccidioidomycosis in two AB strains of inbred mice established that BALB/c mice are significantly more susceptible to pulmonary infection with

Coccidioides immitis than are DBA/2 mice. The

susceptibility of BALB/c mice does not reside in their inability to

mount a delayed-type hypersensitivity response to C. immitis antigen. That is, BALB/c mice manifested footpad hypersensitivity to coccidioidin early during the course

of disease, to a level comparable to that of DBA/2 mice. In contrast to the more resistant DBA/2 mouse strain, however, BALB/c

mice developed anergy by day 15 postinfection. Suppression of the delayed-type hypersensitivity response was not specific for

C. immitis antigen, as evidenced by the finding

that BALB/c mice immunized with mycobacterial purified

protein derivative prior to infection with C.

immitis were suppressed in their footpad response to mycobacterial antigen at day 15 postinfection. Taken together, these results establish that genetically determined susceptibility to this fungus is associated with an acquired suppression of

cell-mediated immune reactivity.

L76 ANSWER 23 OF 25 MEDLINE on STN DUPLICATE 20

ACCESSION NUMBER: 87193089 MEDLINE

DOCUMENT NUMBER: 87193089 PubMed ID: 3552984

TITLE: Serum-mediated suppression of lymphocyte

transformation responses in

coccidioidomycosis.

AUTHOR: Cox R A; Pope R M

CONTRACT NUMBER: AI 18761 (NIAID)

SOURCE: INFECTION AND IMMUNITY, (1987 May) 55 (5) 1058-62.

Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198706

Entered STN: 19900303 ENTRY DATE:

> Last Updated on STN: 19970203 Entered Medline: 19870605

AB Lymphocyte transformation (LT) responses to coccidioidin (CDN) and spherulin were suppressed in 11 (73%) of 15 patients with active coccidioidomycosis when their mononuclear cells were assayed in autologous serum as compared to serum from healthy, CDN skin test-positive subjects. Suppressed LT responses were specific for Coccidioides immitis antigens in 7 (64%) of the 11 patients. Immunoaffinity chromatography of patient sera with Staphylococcus protein A adsorbed the suppressor component(s) and thereby established that suppression was attributed to immunoglobulin G, either alone or complexed with antigen. The possibility that suppression was mediated by immune complexes was examined by adding complexes formed in vivo or in vitro to mononuclear cell cultures of healthy CDN-reactive persons before LT assays. Although complexes prepared in this manner were reactive in an enzyme-linked immunosorbent assay designed to detect Coccidioides antigen-specific immune complexes, no suppression of LT responses was observed. We conclude that serum-mediated suppression of LT responses in coccidioidomycosis is attributed to monomeric and not immune-complexed immunoglobulin G antibody.

L76 ANSWER 24 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on

1984:33723 BIOSIS ACCESSION NUMBER:

DOCUMENT NUMBER: PREV198426033723; BR26:33723

TITLE: CHEMICAL COMPOSITION OF A MYCELIAL AND SPHERULE CELL

WALL ANTIGEN FROM COCCIDIOIDES-IMMITIS.

OLSBERG C A [Reprint author]; COX R A AUTHOR(S):

UNIV TEX HEALTH SCI CENT, SAN ANTONIO, TX, USA CORPORATE SOURCE:

SOURCE: Abstracts of the Annual Meeting of the American

Society for Microbiology, (1983) Vol. 83, pp. F6. Meeting Info.: 83RD ANNUAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY, NEW ORLEANS, LA., USA, MAR.

6-11, 1983. ABSTR ANNU MEET AM SOC MICROBIOL.

CODEN: ASMACK. ISSN: 0094-8519.

DOCUMENT TYPE: Conference; (Meeting)

FILE SEGMENT: BR LANGUAGE: ENGLISH

L76 ANSWER 25 OF 25 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on

STN

ACCESSION NUMBER: 1978:79432 BIOSIS

PREV197815022932; BR15:22932 DOCUMENT NUMBER:

CHEMICAL COMPOSITION OF AN ALKALI SOLUBLE WATER TITLE:

SOLUBLE ANTIGEN FROM COCCIDIOIDES-IMMITIS.

FLEMING W H III; LAND G A; COX R A AUTHOR(S):

Abstracts of the Annual Meeting of the American SOURCE:

Society for Microbiology, (1978) Vol. 78.1978, pp.

CODEN: ASMACK. ISSN: 0094-8519.

DOCUMENT TYPE: Article

FILE SEGMENT: RR

LANGUAGE: Unavailable

FILE 'HOME' ENTERED AT 09:51:03 ON 04 DEC 2003

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score:

Perfect

Run on:

Sequence:

95893, A 305915, 2, Appli 889, App 1638, Ap

Sequence Sequence Sequence

Sequence

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Sequence 16850, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HANDAL GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HANDAL SERON RESEARCH STANO)
TITLE OF INVENTION: WORDER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
SOFTWARE Annomax Sequence Listing Engine vers: 1.1
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
Sequence 5360, Ap
Sequence 71, Appl
Sequence 71, Appl
Sequence 66199, A
Sequence 4623, Ap
Sequence 3626, A
Sequence 36340, A
Sequence 36340, A
Sequence 36340, A
Sequence 36340, A
Sequence 42872, A
                                                                                                                                                   Sequence 27, Applisequence 889, App Sequence 163, App Sequence 19, Appl Sequence 36, Appl Sequence 12310, A Sequence 375, App Sequence 375, App Sequence 378, App Sequence 584, App Sequence 584, App Sequence 584, App Sequence 918, App Sequence 918, App Sequence 918, App Sequence 918, Applis Sequence 918, App Sequence 918, App Sequence 918, App Sequence 918, App Sequence 918, Applis 918
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US-10-027-632-95893
US-10-027-632-95893
US-10-027-632-95893
US-10-027-632-95893
US-10-027-632-95893
US-09-991-936-899
US-09-991-936-899
US-09-991-936-899
US-09-991-936-899
US-10-108-605-36
US-10-198-846-15310
US-09-991-936-975
US-10-198-846-458
US-10-137-473-3
US-10-136-761-4387
US-10-1156-761-918
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ORGANISM: Homo sapiens
FEATURE:
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
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-MODEL=frame+p2n.model-USExth
-MODEL=frame+p2n.model-USExth
-MODEL=frame+p2n.model-USExth
-MODEL=frame+p2n.model-USExth
-MODEL=frame+p2n.model-USExth
-MODEL=frame
-MODEL-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16850, A
                                                                                                                                                                                           November 13, 2003, 12:34:43 ; Search time 214 Seconds (without alignments) 274.896 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                             protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-16850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2169961 segs, 1634102185 residues
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, Ygapext
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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82
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Jatabase :

Score

Result ģ 46

Sequence 30945, A Sequence 185077, Sequence 185078,

Sequence 185079 Sequence 185077

185078, 185079, 203917,

Sequence

Sequence Sequence

Sequence 281505, Sequence 281505,

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GENERAL INDUCEMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Human Genome
FITLE OF INVENTION: Polymorphisms in the Human Genome
FITLE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PRICATION NUMBER: US 60/218,006
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1000-02-24
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-08-09
                                  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 TTTTCCCATATGATGATAGCACTCATAACTGCTGGG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                                                                                     TITLE OF INVENTION: Polymorphisms in the Hun FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/219,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-02-8
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 305915, Application US/10027632 Publication No. US20030204075A9; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6
44.00
83.33
66.67
53.66
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-027-632-305915
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; ORGANISM: Human
US-10-027-632-305915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-95893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-029-386-3150/c
Sequence 3150, Application US/10029386
Sequence 3150, Application US/10029386
Sequence 3150, Application US/10029386
Sequence 3150, Application US/10029386
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT FILING DATE: 2001-12-20
UNIVERNT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3150
LENGTH: 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::||| :::|||||||||||:::
110 CTTCAACACAATCATGCCCTAGTTACTTTGGTAGCAGAAAACCTTGCAACT 60
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 1.0

OTHER INFORMATION: SINSERFOT HIT: G91008, EVALUE 2.00e-19

OTHER INFORMATION: EST HUMAN HIT: AM996853.1, EVALUE 5.00e-79

OTHER INFORMATION: NT HIT: G114764084, EVALUE 3.00e-70
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: Q93008, EVALUE 5.00e-20
; OTHER INFORMATION: NT HIT: G114764091, EVALUE 9.00e-71
; OTHER INFORMATION: EST_HUMAN HIT: AW996853.1, EVALUE 5.00e-73
US-10-029-386-16650
                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-081-935-2 (1-18) x US-10-029-386-16850 (1-168)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
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                                                                                                                                                                                                                                                                                                                                                            46.00
76.47$
52.94$
56.10$
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76.47$
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56.10$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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DB:
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Sequence 99893, Application US/10027632

Seguence 98993, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT PAPLICATION NUMBER: US/10/027, 632
CURRENT PAPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
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SEQUENCE 305915, Application US/10027632

SEQUENCE 305915, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 10802-1129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006
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                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                       3 PheSerHisAlaLeuIleAlaLeuValAlaAlaGly 14
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44.00
83.33%
66.67%
53.66%
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66.67
53.66
                                                                   Percent Similarity:
Best Local Similarity:
Query Fatch:
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Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-027-632-95893
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Alignment Scores:
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DB:
                           Pred. No.:
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APPLICANT: Bunney, William E.
APPLICANT: Bunney, William E.
APPLICANT: Bunney, William E.
APPLICANT: Bunney, William E.
APPLICANT: Cox, David R.
APPLICANT: Cox, David R.
APPLICANT: Cox, David R.
APPLICANT: Cox, David R.
APPLICANT: Li, Jun
APPLICANT: Li, Jun F.
APPLICANT: Li, Jun F.
APPLICANT: The Trustees of The Leland Stanford Junior University
APPLICANT: The Trustees of The Leland Stanford Junior University
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating
TITLE OF INVENTION: Mental Disorders
TITLE REPERENCE: 020885-00021003
FILE REPERENCE: 020885-00021003
FILE REPERENCE: 2002-11-12
FRIOR APPLICATION NUMBER: US 60/339,252
FRIOR APPLICANTION NUMBER: US 60/339,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: chromosome Y ubiquitin-specific cysteine protease OTHER INFORMATION: 9 (USP9Y) (DFFRY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 TITTCCCATATGATGATAGCACTCATAACTGCTGGG 355
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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                    PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1090-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-03-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEC ID NOS: 325720
SEC ID NO 305915
LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10293582
Publication No. US20030175253A1
GENERAL INFORMATION:
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83.33%
66.67%
53.66%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-027-632-305915
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Pred. No.:
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                 Sequence 889, Application US/0991936
; Sequence 889, Application US/0991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisnewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; TITLE OF INVENTION: NUMBER: US/09/991,936
; FILE OF INVENTION: NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: G0/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-991-936-1638

i Sequence 1638, Application US/0991936

j Sequence 1638, Application No. US20030073827A1

i GENERAL INFORMATION:
    APPLICANT: Brandt, Kevin S.
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Wisnewski, Nancy
    TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
    TITLE OF INVENTION: PLAN HEAD, NERVE CORD, HINDGUT AND WALPIGHIAN TUBULE
    TITLE OF INVENTION: WUMBER: US/09/991,936
    CURRENT APPLICATION NUMBER: US/09/991,936
    CURRENT FILING DATE: 2000-04-07
    PRIOR APPLICATION NUMBER: 60/128,704
    PRIOR APPLICATION NUMBER: 60/128,704
    PRIOR PILING DATE: 1999-04-09
    NUMBER OF SEO ID NOS: 1959
    SOFTWARE: Patentin Ver. 2.1
    SEO ID NO 1638
    LENGTH: 549
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                                                                                                                 2)64 CTTCAACAAAATCATGCTTTAGTTACTTTGGTAGCAAAAACCTTGCAACC 2814
                                                                                      1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
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Conservative:
Mismatches:
Indels:
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                                         US-10-081-935-2 (1-18) x US-10-293-582-2 (1-9372)
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; ORGANISM: Ctenocephalides felis
US-09-991-936-889
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'CRGANISM: Crenocephalides felis
US-09-991-936-1638
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43.00
72.22$
50.00$
52.44$
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Best Local Similarity:
Query Match:
DB:
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US-09-991-936-889
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Pred. No.:
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                                                                                                                                                  1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla
                                                                                                                                                                                                                       US-09-894-844-66

Sequence 66, Application US/09894844

Sequence 67, Application US/09894844

Patent No. US20020176873A1

GENERAL INFORMATION:

APPLICANT: Behr, Marcel

APPLICANT: Small, Peter

APPLICANT: Small, Peter

APPLICANT: Wilson, Michael A.

TITLE OF INVENTION: the M. Tuberculosis Complex

FILE REFERENCE: STANIO2CON

CURRENT PFLING DATE: 2001-06-27

PRIOR PILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 137

SSQ ID NO 66

LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-769-734-49/c

Sequence 49, Application US/09769734

Publication No. US20030143666A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ecopia BioSciences Inc.
TITLE OF INVENTION: Genetic Locus for Everninomicin Biosynthesis
FILE REFERENCE: PA 005-US

CURRENT APPLICATION UNBER: US/09/769,734

CURRENT FILING DATE: 2001-01-26

NUMBER 0F SEQ ID NOS: 58

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 49
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0 4
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                 US-10-081-935-2 (1-18) x US-09-991-936-1638 (1-549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-081-935-2 (1-18) x US-09-894-844-66 (1-720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.6
43.00
100.00$
90.91$
52.44$
40.4
43.00
72.22$
50.00$
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; ORGANISM: M. tuberculosis
US-09-894-844-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: M. carbonacea
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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WS-09-712-363-68

WS-09-712-363-68

Sequence 68, Application US/09712363

Pattent No. US20020164588A1

GENERAL INFORMATION:

APPLICANT: Eisenberg, David

APPLICANT: Rotatein, Sergio H.

APPLICANT: Rotatein, Sergio H.

APPLICANT: Marcocte, Edward M.

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

TITLE OF INVENTION: DETERMINING THE FUNCTIONS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 07419-032001

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: 60/126

PRIOR APPLICATION NUMBER: 60/179, 311

PRIOR APPLICATION NUMBER: 60/11, 844

PRIOR APPLICATION NUMBER: 60/116, 593

PRIOR PELING DATE: 1999-03-26

PRIOR PELING DATE: 1999-03-26

PRIOR PELING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/134, 093

PRIOR PELING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/134, 093

PRIOR APPLICATION NUMBER: 60/134, 093

PRIOR APPLICATION NUMBER: 60/145, 124

PRIOR APPLICATION NUMBER: 60/165, 124

PRIOR APPLICATION NUMBER: 60/165, 124

PRIOR APPLICATION NUMBER: 60/165, 124

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-13

PRIOR PILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3042
003
0042
                                                                                                                                                                                                                                                                                             1870 TCCCACTCCGCTGTTTCCCTCGTTGCCGCAGGACTT 1905
                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                              4 SerHisAlaLeuIleAlaLeuValAlaAlaGlyLeu 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                 US-10-081-935-2 (1-18) x US-10-108-605-36 (1-2632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-081-935-2 (1-18) x US-09-712-363-68 (1-3042)
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; Sequence 12310, Application US/10198846
; Deblication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-68
                                                           42.00
91.67%
66.67%
51.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536
42.00
82.35%
52.94%
51.22%
                                                              Score:
Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                      Query Match:
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US-10-108-605-36

Squence 36, Application US/10108605

Publication No. US2002016093441

GENERAL INFORMATION:

APPLICANT: Bradus, Julie

APPLICANT: Bradus, Julie

APPLICANT: Randar, Kim

APPLICANT: Randar, Kim

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

TITLE OF INVENTION: NUCLEIC ACID SEGUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

TITLE OF INVENTION: UNUBER: US/10/108,605

CURRENT FILING DATE: 2002-03-27

PRIOR PLICATION NUMBER: US 09/761,142

PRIOR APPLICATION NUMBER: US 60/176,418

PRIOR PLING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 361

SEQ ID NO 36

LENGTH: 2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LeuValAlaAlaGly 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11115
12
LOCATION: (8)..(1207)
OTHER INFORMATION: ORF 41 (positive strandedness)
OTHER INFORMATION: Incomplete: C-terminus only
NAME/KEY: misc feature
LOCATION: (1213)..(2311)
OTHER INFORMATION: ORF 42 (positive strandedness)
NAME/KEY: misc feature
LOCATION: (3264)..(3511)
OTHER INFORMATION: ORF 43 (positive strandedness)
NAME/KEY: misc feature
LOCATION: (3623)..(4243)
OTHER INFORMATION: ORF 44 (positive strandedness)
NAME/KEY: misc feature
LOCATION: (3623)..(5177)
OTHER INFORMATION: ORF 45 (positive strandedness)
NAME/KEY: misc feature
LOCATION: (5177)..(6094)
OTHER INFORMATION: ORF 46 (negative strandedness)
NAME/KEY: misc feature
LOCATION: (6271)..(6034)
OTHER INFORMATION: ORF 47 (negative strandedness)
NAME/KEY: misc feature
LOCATION: (40703)..(8760)
OTHER INFORMATION: ORF 48 (negative strandedness)
NAME/KEY: misc feature
LOCATION: (40703)..(8760)
OTHER INFORMATION: ORF 48 (negative strandedness)
NAME/KEY: misc feature
LOCATION: (40703)..(8760)
OTHER INFORMATION: ORF 49 (negative strandedness)
COTHER INFORMATION: ORF 49 (negative strandedness)
COTHER INFORMATION: ORF 49 (negative strandedness)
COTHER INFORMATION: ORF 49 (negative strandedness)
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Conservative:
Mismatches:
Indels:
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ORGANISM: Drosophila melanogaster
US-10-108-605-36
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43.00
63.64%
54.55%
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Best Local Similarity:
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Pred. No.:
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; TYPE: DNA; OCRYNEbacterium glutamicum US-09-738-626-3337
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41.00
76.47%
47.06%
50.00%
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Best Local Similarity:
Query Match:
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| Publication No US20030073827A1 |
| GENERAL INPORMATION: |
| APPLICANT: Brandt, Kevin S. |
| APPLICANT: Gaines, Patrick J. |
| APPLICANT: Gaines, Patrick J. |
| APPLICANT: Gaines, Patrick J. |
| APPLICANT: Wisnewski, Nancy TITLE OF INVENTION: FLEA HEAD NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE |
| TITLE OF INVENTION: FLEA HEAD NERVE CORD, HINDGUT AND USES THEREOF |
| TITLE OF INVENTION: PLOCETIC ACID MOLECULES, PROTEINS AND USES THEREOF |
| TITLE OF INVENTION NUMBER: US/09/991,936 |
| CURRENT APPLICATION NUMBER: US/09/543,668 |
| PRIOR FILING DATE: 2000-04-07 |
| PRIOR FILING DATE: 1999-04-09 |
| NUMBER OF SEQ ID NOS: 1959 |
| SEQ ID NO 975 |
| LENGTH: 498 |
APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: PER IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT PILING DATE: 2002-07-18
PRIOR PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PSECS OF WINDOWS VETSION 4.0
SEQ ID NO 12310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HisAlaLeulleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
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111
33
12
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA; ORGANISM: Ctenocephalides felis
US-09-991-936-975
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41.00
68.75%
68.75%
50.00%
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41.00
71.43
64.29
50.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-991-936-975/c
                                                                                                                                                                                                                                                                                                                                                                                  US-10-198-846-12310
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Pred. No.:
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Pred. No.:
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RESULT 17
US-10-198-846-4458/C
i Sequence 4458, Application US/10198846
j Publication No. US2003009974A1
j GENERAL INFORMATION:
j APPLICANT: Lillie, James
j APPLICANT: Action and, Kathleen
j TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
j TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
j TITLE OF INVENTION: THERAPY OF BREAST CANCER
j FILLE REFERENCE: MRI-049
j CURRENT APPLICATION NUMBER: US/10/198,846
j CURRENT FILLING DATE: 2002-07-18
j PRIOR PELLING DATE: 2001-07-18
j NUMBER OF SEQ ID NOS: 14084
j SOFTWARE: FASUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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US-UY-738-626-3337
Sequence 3337, Application US/9938626
PUblication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NATAGAMA, SATOSHI
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: TAYEISHI, MIKRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TAYEISHI, NAOKO
APPLICANT: TAYEISHI, NASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTH VERNIN VERNIN SEQ ID NOS: 7059
SEQ ID NO 3337
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Matches:
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LENGTH: 894
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480 CTGCCTTTGAGCCACCAGCTCGTGCTTCTCCTGGCAATGGGTCTGGTCACAGCA 533
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Chrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REPREMENTE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 584
LEWORTH: 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                           APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WOSHIVKI
APPLICANT: HATTORI, WASAHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                   ; Sequence 4387, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 584, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
41.00
86.67%
60.00%
50.00%
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41.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(1722)
US-10-156-761-4387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                 US-10-156-761-4387/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
US-09-866-050A-584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-866-050A-584
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Pred. No.:
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Fublication No. US20030104419A1

GENERAL INFORMATION:
APPLICANT: GOUID-Rothberg

TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION
THE OF INVENTION UNMBER: US/10/137,473
CURRENT APPLICATION NUMBER: US/09/552,322
PRIOR FILING DATE: 2000-04-19
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                        NAMEKEY: misc_feature
LOCATION: 7, 15, 16, 22, 24, 27, 33, 37, 40, 80, 81, 85, 474, 484,
LOCATION: 501, 512, 527, 543, 550, 551, 553, 555, 564, 567, 584, 587,
LOCATION: 591, 592, 617, 618, 619, 623, 633, 634, 640, 642, 643, 651,
LOCATION: 655, 659, 660, 664, 666, 667, 673, 674, 683, 684, 686
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1218
8
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6
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9
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
41.00
71.43%
64.29%
50.00%
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41.00
66.67$
44.44$
50.00$
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ORGANISM: Murinae gen. sp.
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
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Pred. No.:
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US-10-137-473-3
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US-10-137-473-3
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DB:
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2123 8

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                                                                                                                                                                810 CTGCCTTTGAGCCACCACCAGCTTCTCCTGGCAATGGGTCTGGTCACAGCA 923
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                                                                                                                                                                                                                                                                                            US-10-13-28-801-584

SEQUENCE 584, Application US/10152661

SEQUENCE 100. US20030022835A1

SEQUENCE INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Streaman, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Sleeman, James G.

APPLICANT: Murison, James G.

FILE REFERENCE: 11000.1011c5

CURRENT FILING DATE: 2000-05-20

PRIOR APPLICATION NUMBER: 60/226, 50

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: 60/206, 650

PRIOR APPLICATION NUMBER: 60/206, 650

PRIOR APPLICATION NUMBER: 09/189, 930

PRIOR APPLICATION NUMBER: 09/1069

PRIOR APPLICATION NUMBER: 09/1069

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: 09/1069

PRIOR FILING DATE: 1999-04-29

NUMBER: OF SEQ ID NOS: 725

SEQ ID NO S84

LENGTH: 2123

TYPE: DAA
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Matches:
Conservative:
Mismatches:
Indels:
    Conservative:
                                                                                                                      US-10-081-935-2 (1-18) x US-09-866-050A-584 (1-2123)
                           Mismatches:
Indels:
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                                                                          Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 918, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
  66.67%
44.44%
50.00%
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66.67$
44.44$
50.00$
Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-584
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Pred. No.:
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1168 CTGCAACTGACCACCGCTTGCTTCGTCGAGGGGGGGTGGCCGCC 1218
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: OZAKI, AKKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-4-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7059
SECTIANE: PATENTIN VET: 3.0
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 918
LENGTH: 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHKO
APPLICANT: TATEISHI, NAOKO
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70.59%
47.06%
50.00%
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41.00
76.47%
47.06%
50.00%
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US-10-156-761-918
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-190-305A-70/C

Sequence 70, Application US/10190305A

Publication wo. US2030198621A1

GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, YING
TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REPREMEE: 202-18702, 18702, 002

FILE REPREMER: 202-18702, 18702, 002

CURRENT APPLICATION WHMBER: US/10/190,305A

CURRENT FILING DATE: 2002-07-05

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 70

LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-190-305A-71/C

Sequence 71, Application US/10190305A

Publication No. US20030198621A1

GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: LIAN, Ying C POLYPEPTIDES ENCODING ANTICENIC HIV TYPE B AND/OR
TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION NUMBER: US/10/190, 305A
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 71
                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700356446H1
US-09-294-093B-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 CACCTTCTTCTTGCTCTCCTCGCTGCTGCTGTCGCCGCG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 HisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: TatC22Exonl_2_TV1_C_ZAopt
                                                                                                                                                                                                                                                                                                                                                                               153 ATCCAATTGAATCATGCCCTTCTTGCTCTTGTCAAAGCT 115
                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                  1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAla
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                     52.5
40.00
84.62%
61.54%
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40.00
78.57$
57.14$
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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Pred. No.:
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FEATURE:
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No..
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APPLICANT: Lco, Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/O9/294, 093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
                                                                                                                  32183392 CTTCAGATCGGATACGCCATCATCGGTATCCGCGCCAGCAGGTCTCGCCGCT 3218442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1126427 CTGCAACTGACACCGCTTGCTGCACTTCGTCGAGGCGGGGCTGGCCGCC 1126477
                                                                                  1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
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Matches:
Conservative:
                                         US-10-081-935-2 (1-18) x US-09-738-626-1 (1-3309400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
... LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-081-935-2 (1-18) x US-10-156-761-1 (1-9025608)
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Indels:
                                                                                                                                                                                                                                                                                       APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIRAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BATANOSHI
APPLICANT: BATANOSHI
APPLICANT: OWUREN POLYNUCLEOTIDES
FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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; Patent No. US20010051335A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                           ; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.25e+06
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SOFTWARE:
SEQ ID NO 5360
LENGTH: 228
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
US-09-294-093B-5360/c
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; OTHER INFORMATION: Description of Artificial Sequence: description US-10-190-305A-71
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                                                                                                                                                                        273 CACCTTCTTCTTGCTCTCGCTGCCGGTGCTGTCGCCGCG 232
                                                                                                                                                            S HisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
                                                                           60
8 8 8 8 0 0
                                                                         Length:
Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                      Mismatches:
Indels:
                                                                                                                                          US-10-081-935-2 (1-18) x US-10-190-305A-71 (1-309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(406)
OTHER INFORMATION: n = A,T,C or G
         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                         76.7
40.00
78.57$
57.14$
48.78$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
40.00
75.00%
56.25%
48.78%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATIOUS-10-027-632-66199
                                                                Alignment Scores:
Pred. No.:
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Pred. No.:
LENGTH: 309
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                           FEATURE:
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JEGUERAL INFORMATION:

JEGUERAL APPLICATION NUMBER: US 60/218,006

JEGUERAL FILING DATE: 2000-07-12

JEGUERAL APPLICATION NUMBER: US 60/193,483

JEGUERAL APPLICATION NUMBER: US 60/193,483

JEGUERAL APPLICATION NUMBER: US 60/185,218

JEGUERAL APPLICATION NUMBER: US 60/185,218

JEGUERAL JEGUERATION NUMBER: US 60/167,363

JEGUERAL JEGUERATION NUMBER: US 60/167,363

JEGUERAL JEGUERATION NUMBER: US 60/156,358

JEGUERAL JEGUERATION NUMBER: US 60/146,002

JEGUERAL J
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Facence 4621, Application US/09867701
Facence 4621, Application US/09867701
Facence Wo. US2002013237A1
Facence Wo. US2002013237A1
Facence Wo. US2002013237A1
Facence Wold Composition
Facence Wold Facence
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Matches:
Conservative:
Mismatches:
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Matches:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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Sequence 36340, Application US/10027632

Publication No US20030204075A9

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-04-30

PRIOR PELLING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,218

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/165,363

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: US 60/165,358

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                              Sequence 36266, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20141.756
; CURRENT FILING DATE: 2001-07-30
; PRICH APPLICATION NUMBER: US/09/918,995
; PRICH APPLICATION NUMBER: US/09/215,076
; PRICH APPLICATION NUMBER: US/09/215,076
; RICH APPLICATION NUMBER: US/09/215,076
; SOFTWARE: FREALSEQ for Windows Version 3.0
; SEQ ID NO 36266
                                                                                                                                                                      390 AGCCATCTCCTGATCCTCTTGAAAGCGGCAGGCATCGCT 352
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Matches:
Conservative:
Mismatches:
Indels:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc_feature
LOCATION: (1) ... (445)
OTHER INFORMATION: n = A,T,C or G
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40.00
76.92%
69.23%
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ORGANISM: Homo sapiens
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-09-918-995-36266/c
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US-10-027-632-36340/c
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GENERAL INCOMENTION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Ledentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
PRIOR PRIOR DATE: 1999-08-09
PRIOR PRIOR DATE: 1999-08-09
PRIOR DATE: 1999-08-09
PRIOR DATE: 1999-08-09
PRIOR DATE: 1999-08-09
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SSCTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 36340
LENGTH: 467
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US-10-027-632-36340/c
; Sequence 36340, Application US/10027632
; GENERAL INFORMATION:
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: LOCATION: (1)...(467)

: OTHER INFORMATION: n = A,T,C or G

US-10-027-632-36340
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LOCATION: (1).7.(467)
OTHER INFORMATION: n = A,T,C or G
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56.25%
48.78%
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56.25%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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US-10-081-935-2 (1-18) x US-10-027-632-36340 (1-467)

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Score:
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                                                                                                                                                                                         Sequence 42872, Application US/10027632
Publication No. US20030204075A9
Fubblication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Dolymorphisms in the Human Genome
FILE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/198,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1900-02-24
FRIOR FILING DATE: 1909-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-08-08
FRIOR FILI
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US-10-027-632-42872, Application US/10027632

Sequence 42872, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-04-20

PRIOR PAPLICATION NUMBER: US 60/193,483

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23
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Mismatches:
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Best Local Similarity:
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; ORGANISM: Human
US-10-027-632-42872
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JOSTICAL STATES AND SEQUENCE 2015.05, Application US/10027632

| Publication No. US20030204075A9 | Gequence 2015.05, Application No. US20030204075A9 | Gebome No. US20030204075A9 | Gebome No. US20030204075A9 | Gebome No. US2003020407A9 | Gebome No. US200308 | Gebom
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Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42872
LENGTH: 509
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90.91%
63.64%
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80.00$
46.67$
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Best Local Similarity:
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Query Match:
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                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                          US-10-027-632-42872
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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CRGANISM: Human
US-10-027-632-185077
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Pred. No.:
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                                                            GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PAPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR DATE: 1999-08-09
PRIOR DATE: 1990-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30945, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/235,076
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30945
LENGTH: 513
US-10-027-632-281505; Sequence 281505, Application US/10027632; GENERAL INFORMATION:
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CATION: (1)...(513)
OTHER INFORMATION: n = A,T,C or
US-09-918-995-30945
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-918-995-30945
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Search completed: November 13, 2003, 14:12:16 Job time : 984 secs

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Drosophila melanog Aspergillus oryzae

DNA encoding novel

Drosophila melanog

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Result No.

12645978

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Drosophila melanog

us-10-081-935-1.rng

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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EilSA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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, Jen S, Carter D;
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                                        AAS73006
AAK70862
ABK83564
AAA94724
AAH68302
AAF71300
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ABN20845
AAA94737
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ABL08442
AAC55841
           AAS57170
ABL22998
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AAV05287
AAAS8471
AAH68534
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ABX34289
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ABL08443
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
  20-APR-2001; 2001WO-US12865
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L'maisonneuve J, Zhang Y,
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6: /SIDS1/gcgdata/geneseqf-embl/NA1981.DAT:*
7: /SIDS1/gcgdata/geneseqn-embl/NA1981.DAT:*
8: /SIDS1/gcgdata/geneseqn-embl/NA1981.DAT:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                  hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                               nucleic - nucleic search, using sw model
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AASS9566
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Match
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11-AUG-2000; 2
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                                                                                                                        Sequences AASS9506-AASS9804 represent DNA molecules encoding association and acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions cuesed by P. acnes. The disorders include SAPHO syndrome (Synovitis, acne, pustulosis, hypertosis and colored conditions of medical and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies and therefore treat P. acnes indections. These antibodies and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence. for example, by colypeptides shown in AAUGS618-AAUGS64 and AAUG7799-AAUG7800.

Security of the sequence data for this parent did not form part of the printed consecution in the sequence data for this patent did not form part of the printed precinities. The sequence encodes the specification, but was obtained in electronic format directly from MIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; cermatological; osteopathic; neuroprotectent; ds.
                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                    Claim 1; SEQ ID No 177; 1069pp; English.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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les 34; Conservative
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             WPI; 2001-616774/71.
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September 2019 of the series of the series of the proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include (SAPHO syndrome (Synovitis, acne, pustulosis, hypertosis and solders include cateomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypetides may be used as antigons in the production of antibodies specific for P. acnes proteins. These antibodies can be cased to downregulate expression and activity of P. acnes polypeptides and ctivity of P. acnes polypeptides and ctivity of P. acnes presence, for example, by cancer of an achieve and activity of P. acnes presence are codes the carry in the sequence encodes the carry in the sequence date for determining P. acnes presence, for example, by carry in the sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.2%; Score 25.6; DB 23; Length 34088; 70.8%; Pred. No. 40;
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0
                                                                                                                                                                                                                                                                              Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCAGTICTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34088 BP; 6991 A; 11002 C; 9453 G; 6639 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Psy shcA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                    Claim 1; SEQ ID No 61; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-194160P.
2000US-224604P.
2000US-249548P.
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nes 34; Conservative
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Carr GJ;

Trawick JD,

of •

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential can genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella coneuminae, Pseudomonas aeruginosa and Enterococcus faccalis. The Escherichia is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets for identify proteins used in proliferation, to express these proteins. The proteins can antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery comported in a proteins can be used to screen compounds in rational drug discovery compounds nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part

of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 17459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507 CAGCTCGCTGACCTCCTTGGCCTCGTCGCACGCGACGTCAGCG 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 25; DB 23; Length 1920;
                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                       Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Seq ID No 7958; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                       Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL07659 standard; cDNA; 2016 BP
                           26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
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                                                                                                                                               2001US-269308P
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                                                                                                                                                                                                                                                                       Ohlsen KL,
                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 69.4
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                     Xu HH;
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU36462
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                                                                                                                                                                                                                                                                    Haselbeck R,
Yamamoto RT,
                                                                                                                                                  16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inversion relates to an isolated multiple actu movecure comprising a nucleotide sequence encoding proteins or polypeptides of Pseudomonas Conserved Effector Loci (EEL) and EEL DNA are useful for imparting disease resistance to a plant, by transforming a plant cell with the nucleic acid and regenerating a transgenic plant expresses a heterologous DNA molecule under conditions effective to impart disease a seterologous DNA molecule under conditions effective to impart disease resistance, or by treating a plant with an isolated protein or polypeptide, by applying the protein or polypeptide, under conditions effective to impart disease treated protein or polypeptide, under conditions effective to impart disease resistance to the treated plant. CEL and EEL proteins are useful for causing eukaryotic cell death, by introducing a cytotoxic sequence cells of a patient under conditions effective to cause cell death. By introducing a cytotoxic pseudomonas protein into a eukaryotic cell under conditions effective to cause death of cancer cells of a patient under conditions effective to cause death of cancer cells of a patient under conditions effective to cancer cells of a patient under conditions effective to cancer cells and twus treating the cytotoxic Pseudomonas protein, to the patient involves administering a the cytotoxic Pseudomonas protein, to the patient, where the targetted DNA delivery system delivers the conditions effective comprising a DNA molecule ancoding the cytotoxic Pseudomonas protein, and a second and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid molecule comprising
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                                                                                                                                                                                                                                                          New nucleic acid molecules encoding proteins or polypeptides of
Pseudomonas Conserved Effector Loci and Exchangeable Effector Loci
genomic sequences, for imparting disease resistance to plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa DNA for cellular proliferation protein #452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is expressed in the cancer cells. The present sequence is a DNA encoding Pseudomonas syringae pv. syringae (Psy) shcA protein.
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                           (UYNE-) UNIV NEVADA & COMMUNITY COLLEGE SYSTEM.
(UYNE-) UNIV NEBRASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%; Score 25;
                                                                                                                 Charkowski AO;
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                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 43; 217pp; English.
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(CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 69.4%;
Matches 34; Conservative
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                                                                                                                 Alfano JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                     WPI; 2001-639361/73.
P-PSDB; AAE12589.
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                                                                                                                 Collmer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS54321;
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RESULT 4 AAS54321/

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Gaps

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15; Indels

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Gaps

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The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The nucleic acid can also be used to detect mutations in GPCR genes and gene expression products such as mRNA. AASS7072-AASS7203 represent D. melanogaster G-coupled protein receptor genomic and coding sequences of
                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL0186-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila, G-protein coupled receptor, GCPR, insecticide, diagnostic, mutation detection, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides
                                                                                                                                                                                                                                                                         Query Match
47.7%; Score 24.8; DB 23; Length 4095;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 32; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding Drosophila G-protein coupled receptor, GCPR #50.
 Claim 1; SEQ ID NO 17456; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                    2427 CCCTCACGTTCTCCATGCCCTCGATGACTTCCTCGGCATTG 2470
                                                                                                                                                                                                                                           Sequence 4095 BP; 1151 A; 937 C; 945 G; 1062 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  9 CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 1566 BP; 291 A; 490 C; 437 G; 348 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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18-JUL-2000; 2000US-0618893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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                                                                                                                                                         (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of inscloses, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiol76-ABLio76), expressed DNA sequences (ABLio16176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                      detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 17456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 2016;
                                                                                                                                                                                                                         Claim 1; SEQ ID NO 17459; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590 CCCTCACGTTCTCCATGCCCTCGTCGATGACTTCCTCGGCATTG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2016 BP; 469 A; 511 C; 547 G; 489 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.8; DB:
Pred. No. 52;
0; Mismatches
                                                                  Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL07658 standard; cDNA; 4095 BP
                                                                  PWD,
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72.78;
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11-JUL-2000; 2000US-0614150.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
interactions -
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Best Local Similarity 72.7°
Matches 32, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072).
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                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-656860/75.
                                                                                                     2001-656860/75
                                (PEKE ) PE CORP NY
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                                                                                                                     P-PSDB; ABB63556
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                                                                  Venter JC,
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23-MAR-2000; 2000US-191638P.
18-JUL-2000; 2000US-0618893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation detection; ds
                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                WPI; 2001-656860/75.
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                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200170980-A2
                                                                                                                                                                                                                        interactions
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                                                                          27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel polypeptides (P1) from Drosophila melanogaster having the biological activity of a peptide receptor. Molecules of the invention are used to find new plant protection compounds or insecticides, or to find genes encoding a polypeptide involved in the structure of functionally similar receptors in insects This sequence encodes a Drosophila melanogaster (fruitfly) peptide receptor described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                       New polypeptides from Drosophila melanogaster have biological activity of peptide receptor, useful to find new compounds for plant protection and insecticides
                                                                                                                                                                                        Insect; fruitfly; peptide receptor; plant protection; insecticide; ss.
                           Gaps
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       Length 1566;
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                          Indelg
                                            3 GCAGTTCTCTCACGCTCTCATCGCTCGCTGCCGGCCTCGCCA
                                                                                                                                                                     D. melanogaster peptide receptor encoding cDNA SEQ ID 43.
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                         14;
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        DB 22;
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Pred. No. 59;
0; Mismatches
                         0; Mismatches
       Score 24.6;
Pred. No. 59
                                                                                                                                                                                                                                                                                                                          Schulte T;
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                                                                                                              BP.
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     47.3%;
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                                                                                                                                                  (first entry)
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Best Local Similarity 70.2
Matches 33; Conservative
                         33; Conservative
                                                                                                                                                                                                           Drosophila melanogaster
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               Best Local Similarity
Matches 33; Conser
                                                                                                                                                                                                                                                                                                       (FARB ) BAYER AG
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        Query Match
                                                                                           RESULT 8
AAH49426/c
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical, gene, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 20470; 21pp + Sequence Listing; English.
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Pred. No. 59;
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11-JUL-2000; 2000US-0614150.
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                                                                                                     Drosophila melanogaster
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Matches
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                                                                                                                                          The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The nucleic acid can also be used to detect mutations in GPCR genes and gene expression products such as mRNA, AASS7002-AASS7203 represent D. melanogaster G-coupled protein receptor genomic and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                            Gaps
                                                                                Sixty six Drosophila Melanogaster G-protein coupled receptors (GP useful in the treatment and diagnosis of GPCR-related conditions for identifying GPCR modulators for use as insecticides -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 20467.
                                                                                                                                                                                                                                                                       DB 22; Length 3772;
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                                                                                                                                                                                                                                                                                          14;
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Pred. No. 66;
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                                                                                                                         Claim 4; Page 228-229; 392pp; English
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70.28;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                            Conservative
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                                                 2001-616405/71.
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                                                                                                                                                                                                                                                                                Local Similarity
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                                                             P-PSDB; AAU38972
         CORP
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                                                                                                                                                                                                                                the invention.
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                             Cravchik A;
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         (PEKE ) PE
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production the global expression of genes from FF cells allows the production discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                          Sequence 3772 BP; 933 A; 943 C; 931 G; 965 T; 0 other;
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                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 66;
0; Mismatches
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1 Similarity 70.2%;
33; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-594572/56
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adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF01478 to AAF11847 represents ESTS from Ebusarium venenatum; AAF11248 to AAF11853 represents ESTS from Aspergillus niger; AAF1854 to AAF1878 represents ESTS from Aspergillus oryzae, and AAF14879 to AAF15337 represents ESTS from Aspergillus oryzae, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantiteting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping; gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, s
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                                                                                                                                                                                                                                                                                               Score 24.4; DB 21; Length
Pred. No. 63;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       GATCTCTTACGCCCTCATCGATGACATCGTCGACGGCTTCGC 227
                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                          Sequence 695 BP; 144 A; 199 C; 174 G; 174 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                  6 GITCICICACGCICICATCGCICTCGICGCTGCCGGCCTCGC
                                                                                                                                                                                                              all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #8810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS73006 standard; cDNA; 5484 BP
                                                                                                                                                                                                                                                                                                 46.9%;
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 73.87
Best Local 31; Conservative
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trains to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                  Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25674.
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                                                                                                                                                             DB 23; Length 5484;
                                                                                                                                    Sequence 5484 BP; 1153 A; 1384 C; 1583 G; 1364 T; 0 other;
                                                                                                                                                                                        0; Mismatches 11; Indels
                                                                                                                                                                                                                               4438 TTTGCTGCCTCTCGTCGCTCTCGTCGCCGTCGCC 4397
                                                                                                                                                                                                                 7 TTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC 48
                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                              Score 24.4; I
Pred. No. 80;
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                                                                                                                                                              46.9%;
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17-MAR-2000; 2000US-0190076.
18-APR-2000; 2000US-0198123.
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07-JUN-2000; 2000US-0209467.
28-JUN-2000; 2000US-0214886.
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07-JUL-2000; 2000US-0216647.
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Best Local Similarity
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14-JUL-2000;
26-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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24-FEB-2000;
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2000US-0231414.
2000US-0232080.
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2000US-0241786.
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2000US-0236369
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2000US-0240960.
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2000US-0229344
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2000US-0234998
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                                                     23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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02-077-2000;
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17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249264.
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17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
11-DEC-2000; 2000US-0251989.
11-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251999.
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Rosen CA, Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 25674; 3071pp + Sequence Listing; English.

AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c protein. (I) proteins and polynuclectides may be used to prevent,
c protein. (I) proteins and polynuclectides may be used to prevent,
c ancers and cancer metastases of haematopoietic antigen genomic
c ancers and cancer metastases of haematopoietic antigen genomic
c AXAR87694 represent human immunoh/haematopoietic antigen genomic
c sequences from the present invention. AAX54942 to AAX64950 and AAM82169
cc represent sequences used in the exemplification of the present invention.

Sequence 25913 BP; 5398 A; 6705 C; 7089 G; 6721 T; 0 other;

Gaps 1099 TGCAGTTCCCTCACAGTCTTCACGTTCTCTTCCCTTGCGAAAGCTCCAGT 1148 Query Match

46.9%; Score 24.4; DB 22; Length 25913;
Best Local Similarity 68.0%; Pred. No. 96;
Matches 34; Conservative 0; Mismatches 16; Indels 0; 2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCCGCCTCGCCAGT 51 ò

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA drip analysis as given in the specification, and comparing the expression level in an unactivated to the expression level to an expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chornic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chornic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the expression in a sample of the tissue of gene (s) from GS, where CC level of expression in a sample of the tissue of gene (s) from GS, where CC level of expression of the gene is indicative of inflammation; or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting a tissue having of expression of the gene is indicative of inflammation.

(4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriadis inflammatory disease (e.g. psoriadis respecially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory bowel disease. Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte activation by detecting differential expression
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; alomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in granulocytic cells #135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 135; 114pp; English.
                                              ABK83564 standard; cDNA; 198161 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001WO-US30821.
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                                                                                                                                                                                                                                             14-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-435328/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200228999-A2
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ABK83564/c
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                                                                                                                                                                                                         Gaps
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useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                             25296 recadificercadarcireacericitatecaracerecan 25247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences encoding new auxin transport proteins, useful for modulating root growth of plants and to screen for
                                                                                                                                                                   Score 24.4; DB 24; Length 198161; Pred. No. 1.2e+02;
                                                                                                                                Sequence 198161 BP; 61561 A; 45946 C; 41360 G; 49294 T; 0 other;
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                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice auxin transport protein clone rslln.pk003.n3 DNA sequence
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                                                                                                                                                                                                                                            TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGT
                                                                                                                                                                                                        16; Indels
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                                                                                                                                                                                                        0; Mismatches
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                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                       AAA94724 standard; DNA; 2162 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Auxin transport protein; rice;
                                                                                                                                                                   46.9%;
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                                                                                                                                                                                  Best Local Similarity 68.0 Matches 34; Conservative
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Matches
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AAA94724
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(first entry)

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Corynebacterium glutamicum HA protein nucleotide sequence SEO 1D NO:325
AAF71300 standard; DNA; 732 BP.
                                       30-APR-2001
                   AAF71300;
The present invention provides a number of nucleotide and protein argular the Corpnetorm bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and manlyshing the expression profile or expression amount and a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing manno acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                               S, Hayashi M, Ochiai K, Yokoi H;
Ozaki A;
                                                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
        DB 22; Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO: 3337; 246pp + Sequence Listing; English.
                                                                                                                                              C glutamicum coding sequence fragment SEQ ID NO: 3337.
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Pred. No. 97
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Senoh A, Ikeda M,
                                                                                BP
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                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                               AAH68302 standard; DNA; 609
                                                                                                                                                                                                                                                             18-DEC-2000; 2000EP-0127688
                                                                                                                                                                             organic acid synthesis; ds.
                                                                                                                                                                                                  Corynebacterium glutamicum.
                                                                                                                         (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               Nakagawa S,
Tateishi N,
                                                                                                                         26-SEP-2001
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                                                                                                                                                                                                                                           20-JUN-2001.
                             404
                                                                                                     AAH68302;
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or proteinogenic or nonproteinogenic amino acid (preferred), purine or pryimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine,
Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; sarurated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99DE-1033003.
99DE-1033005.
99DE-1033006.
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99DE-1041379
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0; Mismatches 17; Indels

34; Conservative

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RESULT 18 AAF71300

2 TGCAGTTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCAGTG 52

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cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or hereivecterium. The HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides two major E. maxima gametocyte antigens having molecular weights of 56 and 82 kDa and encoding polynucleotides. The gametocyte antigens can be produced by standard recombinant methodology. The encoding polynucleotides are useful for preparing a vaccine against Eimera tenella, E. acervulina, E. necatrix, E. praecox, E. maxima, E. mitis or E. brunetti infection. The present sequence represents a E. maxima 230 kDa gametocyte antigen cDNA clone.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                              2 TGCAGTTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCAGTG 52
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                                                                                                                                                                                                                   DB 22; Length 732;
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                                                                                                                                                                                                                                                    17; Indels
                                                                                                                                                                               Sequence 732 BP; 183 A; 220 C; 166 G; 163 T; 0 other;
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                                                                                                                                                                                                                 45.8%; Score 23.8; DB 66.7%; Pred. No. 1e+02 ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. maxima 230 kDa gametocyte antigen cDNA.
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                                                                                                                                                                                                                                   Best Local Similarity 66.79
Matches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Belli SI, Smith NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-221605/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BELL/) BELLI S I.
(SMIT/) SMITH N C.
(WALL/) WALLACH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 kDa; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eimeria maxima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003004683-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ59094;
                                                                                                                                                                                                                   Query Match
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   8233333333333
                                                                                                                                                                                                                                                                                          δ
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The present invention describes a nucleic acid (I) comprising a sequence encoding a 250 kbg polypeptide from Sporozoites/Merozoites of sequence encoding a 250 kbg polypeptide from Sporozoites/Merozoites of Sequence comprising the nucleic acid; (2) a host cell comprising the nucleic acid; (3) a host cell comprising the nucleic acid; (4) a transformed copprising the nucleic acid; (5) producing a recombinant 250 kbg cell comprising the nucleic acid; (5) producing a recombinant 250 kbg collypeptide; (6) a recombinant polypeptide; (7) a vaccine against correst acactive antigen; (8) immunising a subject against infection by Eimeria, or a microorganism expressing an immunologically cross-reactive corses-reactive antigen; (8) immunising an immunologically cross-reactive antigen; (9) conferring upon a newborn subject of an avian species conferring upon a newborn subject of an avian species correst and (11) reducing the output of Eimeria oocytes in faces from an avian species having an air sace; (10) a fertilised egg crownth the vaccine; and (11) reducing the output of Eimeria oocytes in faces from an ewborn subject of an avian species (1) has antiparasitic correstive and each be used in a vaccine and in gene therapy. The nucleic correstive correstive sequence represents a 250 kba antigen protein homologous DNA correstive which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid comprising a sequence encoding a 250 kDa polypeptide from sporozoites/merozoites of Eimeria maxima, useful for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                   Eimeria maxima 250 kDa protein homologous DNA sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                       Eimeria maxima; 250 kDa antigen; sporozoite; merozoite; infection; vaccine; antiparasitic; gene therapy; immunodominant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.8; DB 25; Length 7077;
Pred. No. 1.3e+02;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7077 BP; 1814 A; 1985 C; 2165 G; 1113 T; 0 other;
2781 TTCTTCTGCGCACTCATCAATGTCTTGGCAGCCTGCCTCGCCA 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wallach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine against Eimeria infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Fig 7A; 198pp; English.
                                                                                                                      BP.
                                                                                                                  ABZ22977 standard; DNA; 7077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.1%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2002; 2002WO-US21237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2001; 2001US-303670P
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-201556/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WITC/) WITCOMBE D. (SMIT/) SMITH N C. (WALL/) WALLACH M.
                                                                                                                                                                                                                                                                                                                                                                                        WO2003004684-A2
                                                                                                                                                                                                                                                                                                                                Eimeria maxima
                                                                                                                                                                                               10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Witcombe D,
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                         ABZ22977;
                                                                                                  AB222977
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Gaps

Ouery Match 45.8%; Score 23.8; DB 25; Length 7077; Best Local Similarity 72.1%; Pred. No. 1.3e+02; Matches 31; Conservative 0; Mismatches 12; Indels 0;

7 TTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCA 49

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Length 7987;

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The present invention describes a nucleic acid (I) comprising a sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of Eimeria maxima or its homologue or complement. Also describes: (I) a vector comprising the nucleic acid; (2) a host cell comprising the nucleic acid; (2) a producing a recombinant 250 kDa polypeptide; (3) a plasmid comprising the nucleic acid; (5) producing a recombinant 250 kDa polypeptide; (6) a recombinant polypeptide; (7) a vaccine against E. tenella, E. acervulina, E. necatrix, E. praecox, E. maxima, E. mitis or E. brunetti or a microorganism expressing an immunologically cross-reactive antigen; (9) conferring upon a newborn subject against infection by Eimeria, or a microorganism expressing an immunologically cross-reactive antigen; (9) conferring upon a newborn subject of an avian species maternal immunity against infection by Eimeria; (10) a fertilised egg from an avian species having an air sac, where the air sac is incoulated with the vaccine; and (11) reducing the output of Eimeria ocytes in activity and can be used in a vaccine and in gene therapy. The nucleic activity and can be used in a vaccine against E. tenella, E. acervulina, E. necatrix, E. preparing a vaccine against E. tenella, E. acervulina, E. he present sequence encodes a 250 kDa antigen protein, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                / restial
/partial
/product= "250 kDa antigen protein"
/note= "the coding sequence is given as shown in the
figure and any X's in the protein sequence are encoded
by stop codons, no start or stop codons given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid comprising a sequence encoding a 250 kDa polypeptide from sporozoites/merozoites of Eimeria maxima, useful for preparing a vaccine against Eimeria infection
                                                                                                                                                                Eimeria maxima, 250 kDa antigen; sporozoite, merozoite, infection, vaccine, antiparasitic, gene therapy; immunodominant; gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7987 BP; 2022 A; 2217 C; 2370 G; 1378 T; 0 other;
                                                                                                                                 Eimeria maxima 250 kDa protein encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 6; 198pp; English.
                   AB222976 standard; cDNA; 7987 BP
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                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-201556/19.
P-PSDB; ABP56958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WITC/) WITCOMBE D. (SMIT/) SMITH N C. (WALL/) WALLACH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003004684-A2
                                                                                                                                                                                                                           Eimeria maxima.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Witcombe D,
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                                                                                           10-APR-2003
                                                      ABZ22976;
ABZ22976/C
                                                                                                                                                                                                                                                                                 Key
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The present invention describes a nucleic acid (I) comprising a sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of Elmerta maxima or its homologue or complement. Also described: (1) a tenderial maxima or its homologue or complement. Also described: (1) a cetor comprising the nucleic acid; (2) a host cell comprising the nucleic acid; (3) a plasmid comprising the nucleic acid; (4) a transformed cell comprising the nucleic acid; (5) producing a recombinant 250 kDa polypeptide; (6) a recombinant polypeptide; (7) a vaccine against to polypeptide; (8) a recombinant polypeptide; (7) a vaccine against E. mitis corser-reactive antigen; (8) immunising a subject against infection by cross-reactive antigen; (9) conferring upon a newborn subject of an avian species antigen; (9) conferring upon a newborn subject of an avian species antigen; (9) conferring upon a newborn subject of an avian species antigen; (9) conferring upon a newborn subject of an avian species antigen; (1) a fertilised egg from an avian species having an air sac, where the air sac is inoculated with the vaccine; and (11) reducing the output of Eimeria oocytes in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid comprising a sequence encoding a 250 kDa polypeptide from sporozoites/merozoites of Eimeria maxima, useful for preparing a vaccine against Eimeria infection
                                   Gaps
                                                                                                                                                                                                                                                                                                                                Eimeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;
                                   ö
                                                                                                                                                                                                                                                                                              E. maxima immunodominant protein encoding cDNA SEQ ID NO:25.
                                                                                         3011 TTCTTCTGCGCACTCATCATGTCTTGGCAGCCTGCCTCGCCA 2969
                                   Indels
                                                                     49
                                                                     7 TICICICACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "immunodominant protein"
 Score 23.8; DB 25;
Pred. No. 1.3e+02;
                                   12;
                                                                                                                                                                                                                                                                                                                                                vaccine; antiparasitic; gene therapy; gene; ss.
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
231..7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wallach M;
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                                                                                                                                                                          ABZ22984/c
ID ABZ22984 standard; cDNA; 7990 BP.
Query Match
Best Local Similarity 72.1%;
Matches 31; Conservative
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/product=
231..308
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309..7310
                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                   Eimeria maxima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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"module 3 of SorB'

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misc_feature
                                         misc_feature
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                                                                                                                                                                     10-FEB-1998
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AAA58471
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faeces from a newborn subject of an avian species. (I) has antiparasitic activity and can be used in a vaccine and in gene therapy. The nucleic acid is useful for preparing a vaccine against E. tenellah. E. acervulina, E. necatix, E. praecox, E. maxima, E. mitis or E. brunetti infection. The present sequence encodes an E. maxima immunodominant protein, which
                                                                                                            Gaps
                                                                                                                                                                                                                                                                       Polyketide synthase; PKS; biosynthesis; soraphen; SorR; SorA; SorB; SorM; biosynthetic module; beta-ketoacylsynthase; acyltransferase; ketooreductase; beta-ketone processing domain; cytostatic agent; antimicrobial agent; phytopathogenic fungi; transgenic plant; biological control; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "gene product is highly homologous to
type I PKSs that are known to be involved
in the synthesis of polyketide compounds"
                                                                                                                                                                                                                                                         The soraphen biosynthesis gene cluster from Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                             /note= "gene product highly homologous to the reductase domains of type I PKSs such as eryA from Saccharopolyspora erythraea"
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                                                                                       Length 7990;
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0
                                                                   Sequence 7990 BP; 2022 A; 2215 C; 2375 G; 1378 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "yee I PKS genes" type I PKS genes" (*1970..24556
                                                                                                                                       3014 TTCTTCTGCGCACTCATGATGTCTTGGCAGCCTGCCTCGCCA 2972
                                                                                                                            7 TICTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCA 49
                                                                                 / Match
Local Similarity 72.1%; Pred. No. 1.3e+02;
les 31; Conservative 0; Mismatches 12.
                                                 used in an example from the present invention.
                                                                                               Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "module 1 of SorA"
7203..12884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= e
note= "module 3 of SorA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '*tag= d
'note= "module 2 of SorA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of SorB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "module 1 of SorB'
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= i
/note= "module 2 c
30881..35446
                                                                                                                                                                                                AAV05287 standard; DNA; 49377 BP
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/product= SorR
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product= SorB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9871..46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..46318
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                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          927..19874
                                                                                                                                                                                                                                                                                                                                                                                                                                      '*tag= b
'product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942..7115
                                                                                                                                                                                                                                                                                                                                                                 ..760
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9871...
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                                                                                                                                                                                                                                                                                                                                    Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                     21-MAY-1998
                                                                                                                                                                                                                   AAV05287;
                                                                                       Query Match
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Matches
                                                                                                                                                                            RESULT 23
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The present sequence contains a cluster of genes that encode polyketide synthases (PKSs) that are involved in the synthesis of soraphens in Sorangium cellulosum. The proteins encoded by the present sequence are Sorangium cellulosum. The proteins encoded by the present sequence are SorR, SorA, SorB and SorM. SorA and SorB contain biosynthetic modules which contain a beta-ketoacylsynthase, an acyltransferase, a ketoreductase and an acyl carrier protein domain, as well as beta-ketone processing domains. S. cellulosum soraphens are useful as a cytostatic and antimicrobial agent active against phytopathogenic fungi. Soraphen-producing transgenic plants or biological control agents can also be produced, which may reduce crop losses and nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                 "gene product is homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine; thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding Sorangium cellulosum polypeptide(s) - used for, e.g. biosynthesis of soraphen useful as antimicrobial agent against phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19; Length 49377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deprivation for local populations in many parts of the world
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schupp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5048 Gricacceccececrecececrerereses
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Pred. No. 1.6e+02;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GITCICICACGCICICATCGCICTCGICGCIGCCGGCCICGCC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryals JA,
                                                                                                                                 SorB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck JJ, Hill DS, Ligon JM, Neff S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Columns 47-90; 64pp; English.
                                               "module 4 of
                                                                                                     /*tag= 1
/note= "module 5 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                       /*tag= m
/product= SorM
/note= "gene p:
                   /*tag= k
/note= "module
40190..46318
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..40114
                                                                                                                                                        46851..47891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0258261.
96US-0729214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US07954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0764233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3est Local Similarity 72.1
fatches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-158369/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1993;
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transl except= (pos: 1..3, aa: Met)
note= "ORF 15; encodes AAB07571"
00998..52386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ORF 14; encodes AAB07572"
                                     /*tag= a
transl_except= (pos: 1..3, aa: Met)
/note= "ORF 30; encodes AAB07556"
                                                          561.2309
*tag= b
/rag= except= (pos: 1..3, aa: Met)
/note= "ORF 29; encodes AAB07557"
                                                                                                                                 transl except= (pos: 1..3, aa: Met)
                                                                                                                                                                                                                                                                                                                     except= (pos: 1..3, aa: Met)
"ORF 20; encodes AAB07566"
                                                                                                                                                                                                                                                                                                                                                     except= (pos: 1..3, aa: Met)
"ORF 19; encodes AAB07567"
                                                                                                                                                                                                                                                                                                                                                                                    _except= (pos: 1..3, aa: Met)
"ORF 18; encodes AAB07568"
                                                                                                                                                                                                                                                                                                                                                                                                                                          _except= (pos: 1..3, aa: Met)
"ORF 16; encodes AAB07570"
                                                                                                                                                                                                                                        trans1_except= (pos: 1..3, aa: Met)
note= "ORF 23; encodes AAB07563"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "ORF 12; encodes AAB07574"
54187..55824
                                                                                                                                                                                         "ORF 25; encodes AAB07561"
                                                                                                                                                                                                                                                                       note= "ORF 22; encodes AAB07564"
                                                                                                                                                                                                                                                                                                                                                                                                                 note= "ORF 17; encodes AAB07569"
                                                                                                           note= "ORF 28; encodes AAB07558"
                                                                                                                                                                  note= "ORF 26; encodes AAB07560"
                                                                                                                                                                                                               "ORF 24; encodes AAB07562"
                                                                                                                                                                                                                                                                                            note= "ORF 21; encodes AAB07565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encodes AAB07573"
                     Location/Qualifiers
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note= "ORF 13;
                                                                                                                                                                                                                                                                                                                             note= "ORF 2
|5818..37302
                                                                                                                                                                                                                                                                                                                                                                                            note= "ORF 1
9301..47181
                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "ORF 1
9982..51001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3018..54190
                                                                                                                                                                                                                         1010..24666
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                                                                                                                                                                          2291..15491
                                                                                                                                                                                                 5488..21013
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                                                                                           767..3486
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       Streptomyces verticillus.
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The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or poolyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an approgrammer protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic thiazolidine, thiazolime, bithiazolime and bithiazolime, containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07563, AAB07563, AAB07564, AAB07569, AAB07569, AAB07569, AAB07579, AAB07571, AAB07571, AAB07572, AAB07577, AAB07577, AAB07578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 45.8%; Score 23.8; DB 21; Length 58857; Local Similarity 66.7%; Pred. No. 1.7e+02; nes 34; Conservative 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCAGTICTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58857 BP; 7256 A; 25139 C; 19353 G; 7109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C glutamicum coding sequence fragment SEQ ID NO: 7069.
                                                                                                  /transl_except= (pos: 1..3, aa: Met)
/note= "ORF 9; encodes AAB07577"
57583..58857
                                            except= (pos: 1..3, aa: Met)
"ORF 10; encodes AAB07576"
"ORF 11; encodes AAB07575"
                                                                                                                                                                      "ORF 8; encodes AAB07578"
                                                                                                                                                                                                                                                                                                                                                                                               Chen M, Edwards DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 97-136; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH68534 standard; DNA; 309400
                ...56093
                                                              /note= "ORF 1
56090..57586
                                                                                                                                                                                                                                                                                                 06-JAN-1999; 99US-0115435.
05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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                                                                                             /*tag=
/transl
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                                            /transl
 'note=
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                                                                                                                                                                                                       WO200040704-A1
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                CDS
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Ren F;

Zhao QA, F Ghosh M;

oodrich RW, Asundi V, Zhang J, Z; Y, Yamazaki V, Chen R, Wang Z, Wang D, Drmanac RT;

Goodrich RW,

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New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 605; 1012pp + Sequence Listing; English.
                                                                                         05-MAR-2002; 2002WO-US05095.
                                                                                                                       05-MAR-2001; 2001US-0799451
                                                                                                                                                                              Tang YT, Zhou P, Goodr:
Xue AJ, Yang Y, Ma Y,
Wehrman T, Wang J, Wang
                                                                                                                                                                                                                                        WPI; 2002-759812/82
                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                         P-PSDB; ABP69506
                              WO200270539-A2
    Homo sapiens
                                                            12-SEP-2002
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In present invention, by course a minuscal or managed and process from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, coryneform bacterium, coryneform bacterium, coryneform bacterium, coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell-proliferative disorder, neurodegenerative disease, itungus; parkinson's disease, Alzheimer's disease; baccerial; parkinson's disease; Alzheimer's disease; autoimmune disease; autoimmune disease; arthuitis cytostatic; immunomodulator; nootropic; neuroprotective; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.
                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                           mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; genome mapping; gene therapy; food supplement; virus; fungus;
                                                                                                                                                                                                                                                    Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H; Senoh A, Ikeda M, Ozaki A_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218393 TTCAGATCGGATACGCCATCATCGGTATCCGCGCAGCAGGTCTCGCCGCG 218443
Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 309400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGCAGTTCTCTCACGCTCTCATCGCTCGCTGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO: 7069; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                present invention provides a number of nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.8%; Score 23.8; DB 22; Length Best Local Similarity 66.7%; Pred. No. 2e+02; Matches 34; Conservative 0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ11723 standard; cDNA; 1415
                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                         03-AUG-2000; 2000JP-0280988.
                                                                                                                                  18-DEC-2000; 2000EP-0127688
                                                                                                                                                                           07-APR-2000; 2000JP-0159162
                                            Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                WPI; 2001-376931/40.
                                                                        EP1108790-A2
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                                                                                                    20-JUN-2001
                                                                                                                                                                                                                                                   Nakagawa S,
Tateishi N,
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The invention relates to an isolated polynucleotide (1) comprising a nucleotide sequence selected from any of 948 sequences

(Mazilli9-Mazilo66) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP6849) are useful as molecular weight markers, as a food supplement, for generating and indeping, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases

(Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, clers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leinamycin biosynthesis gene cluster; Lmn; open reading frame; ORF; anti-tumour antibiotic; broad spectrum antimicrobial activity; Gram-positive; Gram-negative bacteria; chemical modification; metabolite; apo-carrier protein; holo-carrier protein; tumour; polyketide; hybrid polypeptide/polyketide metabolite; Lnm production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGCAGTTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1415 BP; 337 A; 490 C; 386 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. atroolivaceus leinamycin biosynthesis gene cluster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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es 32; Conservative
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AAD38151 standard; DNA; 145 BP.
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                                                                                               AAD38151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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   4AD38151
                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of the Streptomyces atroolivaceus leinamycin (Lnm) biosynthesis gene cluster containing 1 open reading frames (ORFs -15 through -1, ORFs lnmA through 1 nm2, and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic produced by several Streptomyces species. It exhibits broad spectrum antimicrobial activity against Gram-positive and Gram-negative bacteria, but not against fungl The polypeptides encoded by the Lnm biosynthesis gene cluster ORFs are useful for chemically modifying a molecule in a host cell. The host cell is a bacterium or evagenously supplied metabolite, or an amino acid, and the cell. Including a mammalian, yeast, plant, fungal, or insect cell or exogenously supplied metabolite, or an amino acid, and the polypeptide is a peptide synthetase or amino transferase. The polypeptide is a peptide synthetase or amino transferase. The polypeptides encoded by the Lum gene cluster are useful for converting an apo-carrier protein to a holo-carrier protein. Lnm shows potent modules and/or catalytic domains are useful for making various peptide and/or polyketide, and/or hybrid polypeptide/polyketide metabolites. The Lum gene cluster is useful to upregulate encoded by the ORFs are useful for making various modified Lnm. The Lum production in cells and/or to make various modified Lnm. Computed polyketide metabolites are useful as therapeutic agents, to other polyketide, petrapeutic agents, to there the sequence represents the S. atroolivaceus leinamycin higher cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, ABU11350, ABU11351, ABU11352, ABU11353, ABU11353, ABU11354, ABU11356, ABU11356, ABU11360, ABU11370, ABU11370, ABU11370, ABU11370, ABU11370, ABU11370, ABU11380, ABU11381, ABU11391, ABU11391, ABU11392, ABU11392, ABU11393, ABU11392, ABU11393, ABU11392, ABU11393, ABU11392, ABU11394, ABU11392, ABU11390, ABU11392, ABU11390, ABU11392, ABU11390, ABU11392, ABU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU11387, ABU11388,
ABU11394, ABU11395,
ABU11401, ABU11402,
ABU11408, ABU11409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel gene cluster responsible for synthesis of leinamycin in
Streptomyces atroolivaceus useful for making various peptide and/or
polyketide, and/or hybrid polypeptide/polyketide metabolites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23.6; DB 25; Length 135638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 135638 BP; 18570 A; 49096 C; 49039 G; 18933 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 CGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.1e+02;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU11406,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-018907/01.
P-PSDB; ABU11341, ABU11342, ABU11343, ABU11344, ABU11355, ABU1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU11384,
ABU11391,
ABU11398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU11368, ABU11369, ABU11370,
ABU11375, ABU11376, ABU11377,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU11405,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU11363,
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                                                                                                                                                                                                                                                                                                                        KYOWA HAKKO KOGYO KK
                                                                                                                                                        22-MAR-2002; 2002WO-US08937.
                                                                                                                                                                                                                      26-MAR-2001; 2001US-278935P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosynthesis gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                         Tang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 76.3
Matches 29; Conservative
                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
(KYOW ) KYOWA HAKKO KOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU11382, ABU11383, A
ABU11389, ABU11390, A
ABU11396, ABU11397, A
ABU11403, ABU11404, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU11410, ABU11411.
                                                                                                                                                                                                                                                                                                                                                                                         Cheng Y,
                              WO200277179-A2.
                                                                                               03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU11361,
ABU11368,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Shen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human cytomegalovirus Intron A fragment for use in expression constructs, lacks full-length Intron A sequence, and enhance expression levels when present in expression constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use in expression construct for expressing gene products. Recombinant expression construct for expressing gene products. Recombinant Human cytomegalovirus (hCMV) intron A fragment is useful in expression constructs to express a wide variety of substances including peptides. It is also useful for producing proteins useful for treating a variety of malignant cancers, and for producing proteins useful for prevention, treatment and/or diagnosis of a wide variety of diseases. Recombinant expression construct is used in nucleic acid immunisation and gene therapy. The present sequence is pCOM3 deletion mutant construct intron A fragment used in the invention.
                                                                Cytomegalovirus; CMV; expression construct; gene therapy; cytostatic; human cytomegalovirus; hCMV; malignant cancer; immunisation; intron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to cytomegalovirus (CMV) intron A fragments use in expression construct for expressing gene products. Recombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCAGTTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA
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pCON3 deletion mutant construct intron A fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145 BP; 27 A; 46 C; 27 G; 45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
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                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001WO-US32050
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2000; 2000US-240502P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thudium K, Selby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-452346/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
33; Conserv
                                                                                                                                                                                                                                                               WO200231137-A2.
                                                                                                                                                                                                  Unidentified.
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RESULT 28

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Auxins are plant hormones that influence plant behaviour and development e.g. vascular tissue differentiation, apical development, tropic responses and organ (e.g. flower, leaf) development. The present invention relates to corn auxin transport protein coding sequence and proteins. The present sequence is one such coding sequence. This sequence may be used to modulate root development, e.g. to produce a more robust sequence may be useful for angle or redirect root growth. Also, the present sequence may be useful for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. The protein encoded by the present sequence may be useful for raising specific antibodies, for the detection of auxin transport proteins and to design and/or identify specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitors of auxin transport proteins, potentially useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer; anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences encoding new auxin transport proteins, useful for modulating root growth of plants and to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitomycin biosynthetic gene cluster related alpha amylase orf20.
   Corn auxin transport protein clone cillc.pk001.b7 DNA sequence
                                           Auxin transport protein; corn;
root development; gene mapping; plant breeding; herbicide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 TCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                                                                                                                                                                                Tao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e+02;
                                                                                                                                                                                                                                                                                                                                              Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23.4;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 93; 94pp; English.
                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                              Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC55847 standard; DNA; 2466
                                                                                                                                                                                                              03-MAY-2000; 2000WO-US12061.
                                                                                                                                                                                                                                                    99US-0133040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 45.0%;
1 Similarity 73.2%;
30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces lavendulae,
                                                                                                                                                                                                                                                                                                                                              Orozco EM, Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687647/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                     WO200068389-A2.
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                                                                                                                                                                                                                                                    07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herbicides -
                                                                                                                                                                           16-NOV-2000.
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                                                                                                    Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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AAC55847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) on the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, consecribities, neurodegenerative disorders, cirrhosis of liver, consecribities, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mallitus, systemic storage disease, various immune deficiencies and disorders lester storage disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host diseases, autoimmune inflammacory eye disease. ORFX proteins are also useful for treating burns, inclusions, ulcers, for treating osteoporosis, bence degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibres.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
immune deficiency, immune disorder, infectious disease, autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 450 BP; 86 A; 106 C; 123 G; 133 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 45.0%; Score 23.4; DB 24; 1. Similarity 81.8%; Pred. No. 1.3e+02; 27; Conservative 0; Mismatches 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 10167; 1037pp; English.
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                                                                                                                                                                                         29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                              30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                         Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106308/14.
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                                                                                                                WO200192523-A2.
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                                                                              sapiens.
                                                                                                                                                     06-DEC-2001
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AAA94737
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Gaps

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(DNIM)

(SHER/)

(VARO/) (HEMM/) SHEL/)

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABLi9511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 36251; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAG 50
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Pred. No. 1.6e+02;
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73.2%;
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                                                                                                                                  23-MAR-2001; 2001WO-US09231
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11-JUL-2000; 2000US-0614150
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Best Local Similarity 73.2'
Matches 30; Conservative
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WO200171042-A2.
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                                   10-MAR-2000; 2000WO-US06394.
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                                                                                                                                                                                                                                                                                                                                       SHELDON P C.
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Best Local Similarity
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                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL611840-ABL16175) and the encoded proteins
                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                       Claim 1; SEQ ID NO 19811; 21pp + Sequence Listing; English.
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1 Similarity 67.3%; Pred. No. 1.7e+02;
33; Conservative 0; Mismatches 16;
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2000US-0614150.
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genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical; gene; ss
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WPI; 2001-656860/75.
P-PSDB; ABB64340.
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                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072).
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                                                                                                                                            Sequence 6782 BP; 1899 A; 1548 C; 1559 G; 1776 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9577 BP; 2647 A; 2491 C; 2387 G; 2052 T; 0 other;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                        10 TCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAG
                                                                                                                                                                                                                  0; Mismatches 11;
                                                                                                                                                                                Score 23.4; DB 23;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers
                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                 ABL08442 standard; cDNA; 9577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                Query Match
Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABB64339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
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Sequence 18034 BP; 3203 A; 6345 C; 6150 G; 2335 T; 1 other;

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This invention relates to isolated and purified nucleic acid molecules from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and protein antisathmatic, antiinflammatory, cytostatic, immunomodulatory, and antisathmatic, antiinflammatory, cytostatic, immunomodulatory, and molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to engineer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis
                                                                                                                                                                                                                                                                                    Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotics, anti-inflammatory agents, anti-cancer agents, immune-enhancers, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as protection agents (e.g. fungicides or insecticides) as well as crop PHA monomers synthases. Sequences AAC55782-C55881, AAC55815-C55849 and AAB32485-B32542 represent mitomycin biosynthetic gene cluster DNA AAC55850-C55886 and AAC55862-C55869 represent PCR primers used in the cloning of the mitomycin biosynthetic genes.
                                                                                                                                                                                                                                                                                                      anti-inflammatory; immune-enhancer; immunosuppressant; asthma;
chronic obstructive pulmonary disease; respiratory inflammation;
                8249 CAGTTCTTGCAGGCTCTCGTCGTCGTCGTCGTCGTCGTTG 8201
4 CAGITCICICACGCICTCAICGCICTCGCICGCCGGCCICGCCAGIG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheldon PC;
                                                                                                                                                                                                                                              Complete Mitomycin ORF 11-22 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Figure 23; 399pp; English
                                                                                                                                AAC55841 standard; DNA; 18034 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Varoglu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-2000; 2000WO-US06394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0266965.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                             fungicide; pesticide; ds
                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces lavendulae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sherman DH, Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-601980/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200053737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAO Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
                                                                                                                                                                                                            19. JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000
                                                                                                                                                                    AAC55841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEMM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MINU )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARO/)
                                                                                            RESULT 36
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4.6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. Colynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences to make GM4,6D peptides of the invention.

CMEXTYP42-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding human GM4,6D peptides of the invention.

Specification but was obtained in electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                                                                                            cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsitis; reperfusion injury; stroke; inflection; complex carbohydrate; gene replacement therapy; immunosuppressive; antinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a composition comprising a human GDP-mannose
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                           Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
           Length 18034;
                                             ö
                                               Indels
                                                                                                        11562 CGCTGCCCCCTGATGCCCTCGTCGCCTCCGCCACCGCCA 11602
                                                                                 9 CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA 49
                                                                                                                                                                                                                                                                                                                       Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #12665
Score 23.4; DB 21;
Pred. No. 2e+02;
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 12667; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                             ABX30608 standard; cDNA; 271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumar R;
             45.0%;
73.2%;
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97US-0984246.
98US-0149674.
99US-0333177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-2001; 2001US-0878574
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiasthmatic; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                               30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kriz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-066673/06.
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002110548-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                     11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sullivan F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection
                                                                                                                                                                                                                                                 ABX30608;
                                                 Matches
                                                                                                                                                                            RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                              ABX30608,
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Sequence 271 BP; 76 A; 49 C; 69 G; 76 T; 1 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ9267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder. e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood condition disorders or inflammatory disorders.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from the USFTO web site at seqdata.uspto.gov/sequence.html?DocID=20020082206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease
                                                                                                                                                                                                                                         Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder; ds.
                          Gaps
                          ;
0
 Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.6%; Score 23.2; DB 24; Length 450; 77.8%; Pred. No. 1.5e+02; Live 0; Mismatches 8; Indels 0
                         13; Indels
                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                               8 TCTCTCACGCTCTCATCGCTCTCGCTGCCGGCCTCGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 450 BP; 113 A; 113 C; 159 G; 62 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Law
Query Match
44.6%; Score 23.2; DB 25;
Best Local Similarity 70.5%; Pred. No. 1.4e+02;
Matches 31; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Topper JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID 223; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conley PB,
                                                                                                                                                                                                                  Human ORF112 coding sequence.
                                                                                                                                          ABQ98305 standard; DNA; 450
                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2001; 2001US-0867550
                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-208427P
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mehraban F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEAC/) LEACH M D.
(MEHR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-626554/67.
P-PSDB; ABP63742.
                                                                                                                                                                                                                                                                                                                                               US2002082206-A1.
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                          04-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                         27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach MD,
                                                                                                                                                                  ABQ98305;
                                                                                                                RESULT 38
ABQ98305/c
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 32350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.6%; Score 23.2; DB 23; Length 867; 65.4%; Pred. No. 1.6e+02; vative 0; Mismatches 18; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGCAGITCTCTCACGCTCTCATCGCTCTCGTCGCCGGCCTCGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 32350; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 867 BP; 220 A; 251 C; 207 G; 189 T; 0 other;
                          207 CTCGATCTCGGCGGTCTCGTCGCGGCCTTCCTCGCC 172
     48
13 CACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL60268 standard; cDNA; 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                            ABL26959 standard; DNA; 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                           ABL26959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL60268;
                                                                                                                         RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL60268
ID ABL6
XX
AC ABL6
XX
DT 23-A
                                                                                                                                                    ABL26959
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Gaps

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Best Local Similarity 77.8 Matches 28; Conservative

Query Match

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The invention relates to an expression system (A) that provides increased expression of copper-dependent secreted proteins (I) in eukaryotic cells comprises a gene (II) that encodes (I) and at least one cooper homeostasis gene (III). (A) is used to express enzymes, especially lacese, that require copper as co-factor. (III) transports copper to the present sequence is that of the Trametes versicolor Laccase Jill encoding polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression system for increased production of copper-dependent enzymes, particularly laccase, includes the gene for a copper homeostasis protein
                                                                                     Fungi; Thal; Ctal; copper-dependent secreted protein; copper; laccase;
Trametes ATX1 homologue; copper transporting ATPase; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 44.6%; Score 23.2; DB 24; Length 1563; Best Local Similarity 65.4%; Pred. No. 1.7e+02; Matches 34; Conservative 0; Mismatches 18; Indels 0;
    Trametes versicolor Laccase III encoding cDNA SEQ ID NO 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1563 BP; 271 A; 603 C; 384 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marbach-Ringhandt K, Pfaller R, Uldschmid A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1563
/*tag= a
/product= "Laccase III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 46-48; 58pp; German.
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                                                                                                                                                                                                                   Trametes versicolor.
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P-PSDB; ABB77510.
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Search completed: November 13, 2003, 07:43:16 Job time : 248 secs

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US-09-252-991A-10609/c
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       TYPE: DNA
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Sequence 1,
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
     version 5.1.6
- 2003 Compugen Ltd.
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US-08-252-911A-15702

US-09-252-991A-15654

US-09-266-965-83

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US-09-266-965-75

US-09-252-991A-782

US-09-252-991A-782

US-09-252-991A-782

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                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-443-104-5
US-08-238-130-6
US-08-442-859-5
US-08-398-489-5
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US-09-207-844-1
US-09-252-509-1
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                                                                                                                                                               569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
       GenCore (c) 1993
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c 28 23 44.2 319608 4 US-09-679-409-1 Sequence 1, Appli 29.2.4 43.1 48 2 US-08-169-948B-35 Sequence 35, Appl 31 22.4 43.1 48 2 US-08-364-35 Sequence 35, Appl 32.4 43.1 49 4 US-08-362-452D-35 Sequence 35, Appl 32.4 43.1 702 3 US-09-36-29-2 Sequence 19, Appl 32.4 43.1 702 3 US-09-216-295-2 Sequence 2, Appli 35 22.4 43.1 702 4 US-09-633-084-2 Sequence 2, Appli 36 22.4 43.1 702 4 US-09-633-084-2 Sequence 2, Appli 37 22.4 43.1 702 4 US-09-633-084-2 Sequence 2, Appli 39 22.4 43.1 1050 1 US-08-38-80-11 Sequence 1, Appli 39 22.4 43.1 1050 1 US-08-38-80-11 Sequence 1, Appli 39 22.4 43.1 1050 1 US-08-38-80-11 Sequence 1, Appli 44 22.2 42.7 1140 1 US-08-98-416-751 Sequence 751, Appli 44 22.2 42.7 1140 1 US-08-289-653-1 Sequence 17, Appli 44 22.2 42.7 2845 1 US-08-289-653-1 Sequence 17, Appli 44 22.2 42.7 2845 1 US-08-289-653-1 Sequence 17, Appli 59 22.2 42.7 2845 1 US-08-289-653-1 Sequence 17, Appli 69 22.2 42.7 2845 1 US-08-289-653-1
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ALIGNMENTS

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Sequence 10344; Application US/0925291A
Sequence 10344; Application US/0925291A
Sequence 10344; Application US/0925291A
SEGREAL INFORMATION: Water O. Rubenfield et al.
APPLICANT: Ward O. Rubenfield et al.
APPLICANT: Ward O. Rubenfield et al.
APPLICANT: Ward O. Subbenfield et al.
APPLICANT: Ward O. NUMBER: US/09252,991A
CURRENT PALLICATION NUMBER: US/09252,991A
CURRENT PALLICATION NUMBER: US/0924,190
PRIOR PILING DATE: 1998-02.18
PRIOR PILING DATE: 1999-02.18
PRIOR PRIOR PILING DATE: 1999-02.18
PRIOR PILING DATE: 1999-02.19
PRIOR PILING DATE: 1999-02.19
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PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-10609
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/00/074,788
PRIOR APPLICATION NUMBER: US/00/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Ligon, James M.
APPLICANT: Schupp, Thomas
APPLICANT: Beck, James J.
APPLICANT: Hill, Dwight S.
APPLICANT: Neff, Snezanna
APPLICANT: Ryals, John A.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O.
                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      CITY: Tarrytown
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                  COUNTRY:
                                                     APPLICATION NUMBER:
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Pred. No. 8.1;
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                                                                                        Version
                                                                                                                                                                                                                                                             Box 2005
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TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
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LOCATION: 19871.46318
OTHER INFORMATION: /prod
OTHER INFORMATION: /note
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19870.24556
                                               FEATURE:

NAME/KEY: misc feat
LOCATION: 35528..40
OTHER INFORMATION:
                                                                                                                                                                                                    FEATURE:

NAME/KEY: misc_feature

POCATION: 24638..30820
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NAME/KEY: misc_feature
7203.12884
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LENGTH: 49377 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 08-JUN-
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OTHER INFORMATION: /product= "module 3"
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LOCATION: 383..760
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OTHER INFORMATION: /note
OTHER INFORMATION: the 1
OTHER INFORMATION: Sacch
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ORIGINAL SOURCE:
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                                                                                                                    FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: 30881..35446
OTHER INFORMATION: /product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
NAME/KEY:
LOCATION:
                                                                                                                                                                                              OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                    OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 7203..1: OTHER INFORMATION:
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LOCATION: 927..19874
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                                                                   misc_feature
35528..40114
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misc_feature
40190..46318
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                                                                                                                                                                                                                                                                                                                                        /product= "SorB"
/note= "Gene product is highly homologous to type I PKS
                                                  /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product = "SorA"
/note = "Gene product is highly homologous are known to be involved in the synthesis compounds."
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/note= "This gene encodes a protein that is highly homologo
the reductase domains of type I PKSs such as eryA from
Saccharopolyspora erythraea."
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                        Sequence 15674, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15702
SEQ ID NO 15674
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (669)
OTHER INFORMATION: Identity of nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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/note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin."
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Pred. No. 25;
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Pred. No. 29;
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APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: He, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION. Mitomycin biosynthetic ger
TITLE OF INVENTION. Mitomycin biosynthetic ger
TITLE OF INVENTION. MITOMEER: US/09/266, 965
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER APPLICATION NUMBER: DE 08/624/11279
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
NUMBER OF FOR TO NOC.
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; LOCATION: (415)
; OTHER INFORMATION:
US-09-252-991A-15656
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15656
                                                                                                                                                                                                                                                                                                Sequence 83, Applica Patent No. 6495348 GENERAL INFORMATION:
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GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (571)
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Pred. No. 26;
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Pred. No. 25;
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SEQ ID NOS: 145

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Patent No. 6495348

GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Varoglu, M
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: He, M
APPLICANT: He, M
CONTROL OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
EARLIER FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1993-10-07
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
EARLIER FILING DATE: 1993-10-07
SERIER FILING DATE: 1993-10-07
EARLIER FILING DATE: 1993-10-07
                                                                                                                                                                                                                 US-09-252-991A-782/c; Sequence 782, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
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; ORGANISM: Streptomyces lavendulae
US-09-266-965-83
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SEQ ID NO 83
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              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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OTHER INFORMATION: n is a
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LOCATION: (302)..
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TYPE: DNA
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SEQ ID NOS:
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73.2%;
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73.2%;
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Pred. No. 21
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US-07-661-610C-13
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LENGTH: 201
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                                                          Matches
                                                                        Query Match
Best Local
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Best Local :
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                    FILING DATE: 19910228
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5292643man
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 229
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/661,610C
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
OBLON, SPIVAK, McCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Toyoda, Hideyoshi
APPLICANT: Utsumi, Ryutaro
APPLICANT: Obata, Kazuaki
                                                                                                                                   TOPOLOGY: un MOLECULE TYPE:
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Vity
                                                                                                                                                            LENGTH: 1038 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 Jei
CITY: Arlington
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                                                                       1 44.6%;
Similarity 65.4%;
Application US/07661610C
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1755 Jefferson Davis Highway, Fourth Floor
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                                                       ; Score 23.2; D; Pred. No. 29; 0; Mismatches
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Pred. No. 24;
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                                                                                     DB 1;
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64
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RESULT 12 US-08-443-104-6

; Sequence 6, Application US/08443104
; Patent No. 5691162

GENERAL INFORMATION

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RESULT 13
US-08-442-859-6
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                             APPLICANT: Madden, Mark
APPLICANT: Moyer, Donna L.
APPLICANT: Fuglasng, Claus
APPLICANT: Branner, Sven
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 10
                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                      APPLICANT:
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LENGTH: 1899 base pairs
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APPLICATION NUMBER: US 00
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM
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APPLICANT: Branner, Sven
TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED
TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: SI
                                COUNTRY:
                                                                                STREET:
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TELEPHONE: 212-878-9655
TELEPHONE: 212-0.
TELEPHONE: 212-0.
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REGISTRATION NUMBER: 34,00
REFERENCE/DOCKET NUMBER:
                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/01
FILING DATE: 17-MAY-1995
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                 10174-6401
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                                                                           405 Lexington Avenue,
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                                USA
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Madden, Mark
                                                                                            No. 58077290 No. 5807729disk of No. 5807729th America, Inc
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Pred. No. 32;
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RESULT 14
US-08-398-489-6
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION SATA:
APPLICATION SATA:
APPLICATION 125/08/398,489
FILING DATE: 03-MAR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                               ATTORNEY/AGENT INFORMATION:
NAME: AGYIS Dr., Cheryl H.
REGISTRATION UMBER: 34,086
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shuster,
APPLICANT: Madden, N
APPLICANT: Moyer, Do
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 58437
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELECPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03=MAR-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/398,489
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                                TELEPHONE:
                                                                                                                                                                                                                                                                                                           ZIP: 10174-6401
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                                                                                                                                                                                                                                                                                                                                                             CITY: New York
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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COMPUTER: I
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                 : 212-867-0123
212-878-9655
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Branner, Sven
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Moyer, Donna L.
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ilarity 65.4%;
Conservative
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15 Lexington Avenue, 64th Floor
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SYSTEM: PC-DOS/MS-DOS
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                                                                                  34,086
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Pred. No. 32;
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Best Local S
Matches 34
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Best Local Similarity 65.4
Matches 34; Conservative
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                                                                                                                                                                                                                                         TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10174-6401

ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
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                                                                                                                                           TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,489
FILING DATE: 03-MARCH-1995
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APPLICATION NUMBER: U
FILING DATE: 04-MAY-
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                     NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,08
REFERENCE/DOCKET NUMBER: 4
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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STATE: New York
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                                                                                                                                                                                                         LENGTH:
                                                                              Similarity
                                                                                                                                                                                        nucleic acid
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                               ATGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG 52
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ATGCGTTTCTCCGACTCTCTCCTCATCGGCCTATCCAGCCTCGCTGGTG 52
                                                                                                                                                                                                      1899 base pairs
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linear
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ER: 4180.204-WO
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Pred. No. 32;
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Pred. No. 32;
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US-08-443-104-5
                                                                                                                                               US-08-238-130-6
                                                                                                                                                                 RESULT 17
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                                                                                                                 Patent No.
                                                                                                                  Sequence 6, Applic Patent No. 5702934
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Patent No. 5691162
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Best Local Similarity
                                                                                                    GENERAL
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INFORMATION FOR SEQ ID NO:
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                         APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,489
FILING DATE: 03=MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Agris Dr., Cheryl H
REGISTRATION NUMBER: 34,08
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
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NAME: Agris Dr., Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUMBER OF SEQUENCES:
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TELEPHONE: 212-878-9655
TO TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0: FILING DATE: 17-MAY-1995
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                                                                                                    INFORMATION:
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Moyer, Donna L.
Fuglsang, Claus
Branner, Sven
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Christensen, Tove
Jorgensen, Birgitte B.
Shuster, Jeffrey R.
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                                                      Jorgensen, Birthe R.
                                                                    Hastrup, Sven
Branner, Sven
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Pred. No. 32;
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APPLICANT: APPLICANT:

Madden, Mark Moyer, Donna L. Fuglsang, Claus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICANT: Shuste
APPLICANT: Madden
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   APPLICANT: Moyer, Donna L.
APPLICANT: Fuglsang, Claus
APPLICANT: Branner, Sven
TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED
TITLE OF INVENTION: ACTIVITY
                                                                                                    CORRESPONDENCE ADDRESS ADDRESSEE: No. 5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
DK 522/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,130
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NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
COMPUTER READABLE FORM
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FILING DATE: 05-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl I
REGISTRATION NUMBER: 34,0
                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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LOCATION:
                                                    STATE: New York
                                 COUNTRY:
                                                                                     STREET:
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ZIP: 10174-6401
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                10174-6401
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                                                                                 405 Lexington Avenue,
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405 Lexington Avenue, 64th Floor
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Moyer, Donna L.
Fuglsang, Claus
                                     USA
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join(1..363, 416..802, 856..1821, 1870..2049)
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                                                                                                58077290 No. 5807729disk of No. 5807729th America, Inc
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Pred. No. 32;
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                                                                                     64th Floor
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US-08-398-489-5
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                                                                                                                                ZIP: 10174-6401

ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,489
FILING DATE: 03-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-867-01;
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                              ATTORNEY/AGENT INFORMATION:
NAME: AGYL'S Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 411
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 03=MAR-1995
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APPLICATION NUMBER: US/0:
FILING DATE: 17-MAY-1995
CLASSIFICATION: 252
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                     ANUNKESSEE: No. 58437530 No. 5843753disk of No. 5843753th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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REGISTRATION NUMBER: 34,08
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34; Conservative
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Branner, Sven
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                                   212-867-0123
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                                                                  4180.010-US
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RESULT 21
US-09-207-844-1
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US-08-894-772-1
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US-08-894-772-1
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Best Local Similarity 65.7
34; Conservative
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                                                                                                                     Matches
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LENGTH: 2052 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                     TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 27-AUG-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2052 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                 NAME: Gregg, Valeta A. REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                     Local
                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                     Similarity
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Y: U.S.A.
                                                                                     ATGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                               TYPE:
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                                                          ATGCGTTTCTCCGACTCTCTCCTCCTCATCGGCCTATCCAGCCTCGCTGGTG
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                                                                                                                     Conservative
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Pred. No. 32;
                                                                                                                                   Score 23.2;
Pred. No. 32;
                                                                                                                   Mismatches
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US-09-252-509-1
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                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09252509 Patent No. 6352841
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Best Local
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                                                     SEQ ID NO 1
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                                                                                                                    PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0
PRIOR APPLICATION NUMBER:
DBIOR BETTTE
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,509
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6352841el Host Cells and Methods TITLE OF INVENTION: Producing Proteins FILE REFERENCE: 4920.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 1:
                                                                      PRIOR FILING DATE: 1999-09-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION UNMBER: 08/894
APPLICATION NUMBER: 08/894
FILING DATE: 27-AUG-1997
ATTORNEY/AGENT INFORNATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,12
REFERENCE/DOCKET NUMBER: 4
                   LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                           APPLICANT:
ORGANISM: Fusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,844
FILING DATE:
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COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 405 Lexi
CITY: New York
STATE: New York
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                                      2052
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405 Lexington Avenue, Suite 6400
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              PCT/DK97/00397
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Pred. No. 32;
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; TOPOLOGY: 1; MOLECULE TYPE: PCT-US95-05534-5
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PCT-US95-05534-5
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Best Local Similarity 65.4
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Applicati
GENERAL INFORMATION:
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: AGYLS Dr., Cheryl H.
REGISTRATION UNMBER: 34,086
REFERENCE/DOCKET NUMBER: 4180
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHAX: 212-878-9655
                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/ncer.
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LOCATION:
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                                                                                                                                                                                                                                                                             PRIOR APPLICATION UNMBER: US 08/238/108
FILING DATE: 04-MAX-1994
CLASSIFICATION UNABER: US 08/398,489
FILING DATE: 03-MARCH-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NO TITLE OF INVENTION: ACCUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 405 Le
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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(55)...(784
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(785) ... (20
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   44.6%;
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Pred. No. 32;
0; Mismatches
Score 23.2; DB 5; Pred. No. 32;
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             Length 2052;
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US-07-661-610C-1
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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5392643man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-01/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5437 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Patent No. 529264
                                                    FEATURE:
NAME/KEY:
LOCATION:
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FEATURE:
NAME/KEY:
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FEATURE:
NAME/KEY:
                                                                                                                              LOCATION: FEATURE:
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            ORGANISM:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSER: OF SEQUENCE ADDRESS:
                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Toyoda, Hideyoshi
APPLICANT: Utsumi, Ryutaro
APPLICANT: Obata, Kazuaki
FEATURE
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                                                                                                                                                                          PEATURE
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STATE: 22202
            NAME/KEY:
LOCATION:
                                                                                                 NAME/KEY:
LOCATION:
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                                                                                                                                                                                      LOCATION
                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                             NAME/KEY:
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                                                      CDS
2314..3354
                                                                                                 RBS
2301..2304
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1836..1839
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519..
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            3405..3409
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RESULT 26
5202236-12/c
;Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
; APPLICANT: MACCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
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                                                                                                        5202236-12
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                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PFALLER, Rupert
TITLE OF INVENTION: EXPRESSION SYSTEM FOR PRODUCTION OF PROTEINS
FILE REFERENCE: PFALLER ET AL.-2 (PCT)
CURRENT APPLICATION NUMBER: US/09/647,492A
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 5762
TYPE: DNA
ORGANISM: Trametes versicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09647492A Patent No. 6551797 GENERAL INFORMATION:
                                         Query Match
Best Local Similarity
Matches 29; Conserv
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Best Local
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                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                 FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24 NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 39
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LOCATION:
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                                                                                                                       LENGTH: 3903
                                                                                                                                                  FILING DATE: 13-SEP-1984
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11 CTCACGCTCTCATCGCTCGCTCGCCGGCCTCGCCA 49
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Similarity 65.4%;
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                                              Conservative
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3414..4040
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Pred. No. 36;
0; Mismatches
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Pred. No. 36;
0; Mismatches
                                                           Score 23; DB
Pred. No. 40;
                                             Mismatches
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                                                                        Length 3903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5762;
                                             Indels
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APPLICANT: ESSIOUX, LAUTENT
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR APPLICATION NUMBER: US 60/146,384
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR APPLICATION NUMBER: US 60/162,384
PRIOR APPLICATION NUMBER: US 60/162,384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 319608
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 31..1107
                                                                    NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon
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LOCATION: 18778..18862
OTHER INFORMATION: exor
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OTHER INFORMATION: e:
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NAME/KEY: exon
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LOCATION: 25593..
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LOCATION: 14877..14920
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NAME/KEY: exon
LOCATION: 64666..64812
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                                                                                                                                                                         29388..29502
DRMATION: exon
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                                                                          g35018 gene
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NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis
                                                                       NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2
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NAME/KEY: exon
CATION: 215819..215975
FORMATION: exon Rbis
NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement
                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER_INFORMATION: 3'regulatory region g34872 gene
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LOCATION: 65505..65853
OTHER INFORMATION: exon G
FEATURE:
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LOCATION: 217027..217061
OTHER INFORMATION: exon Q1
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LOCATION: 215819..215941
OTHER INFORMATION: exon R
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LOCATION: 216836..216915
OTHER_INFORMATION: exon V
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LOCATION: 214676..214793
OTHER INFORMATION: exon T g35030 gene
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LOCATION: 201188..201234
OTHER INFORMATION: exon
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OTHER INFORMATION:
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LOCATION: 216661..216952
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LOCATION: 215702..215746
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LOCATION: 65854..67854
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                                                           Query Match
Best Local Sim
Matches 32;
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LOCATION: 290652..292652
OTHER_INFORMATION: 3'regulatory
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LOCATION: 240528..240644
LOCATION: EXONMATION: EXON
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NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon /
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LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
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LOCATION: 237406..237428
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NAME/KEY: exon
LOCATION: 234174...234321
OTHER INFORMATION: exon O complement g34872 gene
                                                                                                                     NAME/KEY: exon
LOCATION: 292653..292841
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory
                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon
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LOCATION: 240528...241685
OTHER INFORMATION: exon M1 complement g34872 gene
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LOCATION: 240528..240994
OTHER INFORMATION: exon M692
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LOCATION: 240528..240617
OTHER INFORMATION: exon
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LOCATION: 240528..240596
OTHER INFORMATION: exon |
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LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872
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OTHER INFORMATION: exon
FEATURE:
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184156 CAGTTCACTAAGGCACTCAGCTCTGTCCTTGCTGTGGTCATACCCAG 184110
                     4 CAGTTCTCTCACGCTCTCATCGCTCTCGTCGCCGGCCTCGCCAG
                                                                            Similarity
                                                            Conservative
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Pred. No.
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                                                                                     Length 319608;
                                                            Indels
                               50
                                                            0
                                                           Gaps
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RESULT 28 US-09-679-409-1/c ; Sequence 1, Application US/09679409 ; Patent No. 6555316

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APPLICANT: Bougueleret, Lydie
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: 53.US15.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT FILING DATE: 09/539,333
PRIOR APPLICATION NUMBER: 09/539,333
PRIOR FILING DATE: 1200-03-03
PRIOR FILING DATE: 1200-03-03
PRIOR FILING DATE: 1200-12
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEO ID NOS: 134
SOFTWARE: Patent.pm
SEO ID NO 1
LENGTH: 319608
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APPLICANT: Cohen, D.
APPLICANT: Blumenfe
APPLICANT: Chumakov
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NAME/KEY: exon

LOCATION: 201123..201560

OTHER INFORMATION: exon S2

NAME/KEY: exon

LOCATION: 214676..214793

OTHER INFORMATION: exon T

NAME/KEY: exon

LOCATION: 215702..215746

OTHER INFORMATION: exon U
LOCATION: 246273...247802
OTHER INFORMATION: exon Z
NAME/KEY: misc feature
LOCATION: 247803...249803
OTHER INFORMATION: 3'regula
NAME/KEY: allele
LOCATION: 8316
                                                                                                                                                                      NAME/KEY: exon
LOCATION: 241072..241291
OTHER INFORMATION: exon X
NAME/KEY: exon
LOCATION: 244353..244561
OTHER INFORMATION: exon Y
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 227655.227736
OTHER INFORMATION: exon V4
NAME/KEY: exon
LOCATION: 238715.238919
OTHER INFORMATION: exon V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 216836..217077
OTHER INFORMATION: exon V2
NAME/KEY: exon
LOCATION: 217671..217764
OTHER INFORMATION: exon V1
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 201123..201234
OTHER INFORMATION: exon S
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NAME/KEY: misc feature
LOCATION: 199122..201122
OTHER INFORMATION: 5'regulatory region
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LOCATION: 240440..241153
OTHER INFORMATION: exon W2
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LOCATION: 216836..216994
OTHER INFORMATION: exon V
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: exon W
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LOCATION: 240440..240673
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Chumakov, Ilya
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                                      3'regulatory region
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INFC	INFORMATI	INFORMATI	INFORMATI	INFORMATI	INFORMATI	INFORMATI	- H O F	ION: 20413 INFORMATI	TION: R INF /KEY:	LOCATION: 202679 OTHER INFORMATION: NAME/KEY: allele	20265 XMATI allel)RMATI	OTHER INFORMATION: NAME/KEY: allele		1733E)RMATI allel	17081)RMATI	16897 DRMATI	16087 ORMATI allel	1606 DRMAT alle	0728 MATI 11el	95396)RMAT1 alle1	65485)RMATI allel	ATION: ER INFO E/KEY:	ER INFORM
lymo	8-251-322 : polymorphic base A or G	8-292-198 : polymorphic base A or G	8-293-130 : polymorphic base A or G	8-295-125 : polymorphic base C or T	8-295-248 : polymorphic base A or C	99-24644-194 : polymorphic base A or G	8-252-190 : polymorphic base C or T	8-296-213 : polymorphic base A or T	8-299-128 : polymorphic base A or T	8-300-193 : polymorphic base A or G	8-300-221 : polymorphic base A or G	8-303-235 : polymorphic base A or G	99-24658-410 : polymorphic base A or G	99-5919-215 : polymorphic base A or G	99-5862-167 : polymorphic base A or G	99-16100-147 : polymorphic base A or G	99-7652-162 : polymorphic base A or G	99-24634-108 : polymorphic base A or T	99-24639-163 : polymorphic base A or C	99-24656-260 : polymorphic base A or G	99-31960-363 : polymorphic base A or G	8-128-33 : polymorphic base C or T	99-27935-193 : polymorphic base G or C	99-27943-150 : polymorphic base G or C

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RESULT 29
US-08-169-948B-35
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                                                                                         Sequence 35, Application US/08169948B Patent No. 5861271
                                                                                                                                                                                                                             Matches
                                  GENERAL INFORMATION:
APPLICANT: Fowler, Timot
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kat
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 8-279-197
                                                                                                                                                                                                                                                                                NAME/KEY: allele
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 8-278-289
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 8-281-248
                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 8-281-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 211132
OTHER INFORMATION: 8-282-92
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OTHER INFORMATION: 8-282-174
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OTHER INFORMATION: 8-283-176
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OTHER INFORMATION: 8-287-86
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LOCATION: 211315
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OTHER INFORMATION: 8-282-260
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LOCATION: 210583
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LOCATION: 210486
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OTHER INFORMATION: 8-283-278
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NAME/KEY: allele
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 TITLE OF INVENTION:
                APPLICANT:
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                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                        Similarity
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             Larenas,
                                                               Fowler, Timothy
                                                                                                                                                                                                                            Conservative
                          Collier, Katherine
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68.1%;
No. 5861271el Cellulase Enzymes
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                                        Kathleen
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Pred.
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RESULT 30
US-08-448-873-35
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Patent No. 5
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                         APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Kathlerine A.
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5874276el Cellulase
TITLE OF INVENTION: For Their Expressions
                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
CLASSIFICATION: 435
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742,7536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                FILING DATE:
CLASSIFICATION:
                                                 APPLICATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                        COUNTRY:
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                                                                                                                                   Floppy disk
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66.7%; Pred. No. 38;
tive 0; Mismatches
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; TOPOLOGY: 1
; MOLECULE TYPE:
US-08-382-452D-35
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                                                                                                                                      NAME: Christopher L. Stone
REGISTRATION NUMBER: 36,696
REFERENCE/DOCKET NUMBER: GC226-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 32; Conserv
Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEPHONE: (415) 742-7217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Collier, Katherine D.
APPLICANT: Larenas, Edmund A.
TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS
TITLE OF INVENTION: FOR THEIR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Clarkson, Kathleen A. APPLICANT: Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                    STRANDEDNESS:
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                                                                                                      nucleic acid
DEDNESS: single
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                                                                   DNA (genomic)
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Pred. No. 38;
Score 22.4;
Pred. No. 38;
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                DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
              Length 48;
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US-08-507-362A-19
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                                                                                                                                             US-09-146-770-2
                                                                                                                                                                  RESULT 33
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             Sequence 2, Application US/09146770
Patent No. 6187732
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
FILE REFERENCE: GC546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6562340
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/146,770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Castaneda, Janet
REGISTRATION NUMBER: 33,228
REFERENCE/DOCKET NUMBER: GC226-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/507,362A FILING DATE: 27-Oct-1995 CLASSIFICATION: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: An Enzyme Feed Additive and Animal Feed Including It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bedford, Michael
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 49 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 846-4
TELEFAX: (650)845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morgan, Andrew
Fowler, Timothy
                                                                                                                                                                                                                                                                                                             43.1%;
66.7%;
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Pred. No. 38;
                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                          ; SEQ ID NO 2
; LENGTH: 702
; TYPE: DNA
; ORGANISM: T. longibrachiatum
US-09-633-084-2
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US-09-633-084-2
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Best Local S
Matches 32
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                   Patent No. 6407046
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 702
TYPE: DNA
ORGANISM: Trichoderma longibrachiatum
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GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 702
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                   Matches
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                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/633,084
CURRENT FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 09/146,770
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mitchinson, CAPPLICANT: Wendt, Dan J.
TITLE OF INVENTION: NO.
FILE REFERENCE: GC555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding TITLE OF INVENTION: Such EGIII Compositions and Methods
                                                                                                                                                                                                                                                                            FILE REFERENCE: GC546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 702
TYPE: DNA
ORGANISM: T. longibrachiatum
                                                               Local
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5. 6407046
1 ATGCAGTTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCC
                                             l Similarity
32; Conserv
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                                                Conservative
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66.7%;
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                                                              Score 22.4;
Pred. No. 51;
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Pred. No. 51;
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Pred. No. 51;
                                             Mismatches
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; SEQ ID NO 2
; LENGTH: 702
; TYPE: DNA
; ORGANISM: T.
US-10-261-997-2
            Patent No. 5475101

GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Mo
TITLE OF INVENTION: EG III Cellulase
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                  RESULT 38
US-08-032-848C-11
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US-10-261-997-2
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TYPE: DNA
; ORGANISM: T. longibrachiatum
US-10-075-872-2
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APPLICANT: Fowler, Timothy
TITLE OF INVENTION: Mutant
TITLE OF INVENTION: Such E
FILE REFERENCE: GC546
                                                                                                                                                                      Sequence 11, Application US/08032848C Patent No. 5475101
                                                                                                                                                                                                                                                                                                                                       Matches
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Patent No. 6500211
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/261,997
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/075,872
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mutant EGIII Cellulase, DNA TITLE OF INVENTION: Such EGIII Compositions and FILE REFERENCE: GC546
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                  32;
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Pred. No. 51;
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Pred. No. 5
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ADDRESSEE: Genencor International STREET: 180 Kimball Way CITY: South San Francisco

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Best Local (
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APPLICATION NUMBER: US/08/438
FILING DATE: May 10, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7555
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CONTROL OF THE PROPERTY OF THE PROPERTY APPLICATION DATA:
CONTROL OF THE PROPERTY OF THE PROP
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of EG
TITLE OF INVENTION: III Cellulase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International
STREET: 180 Kimball Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenas, Edward
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NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: MAR 17 199
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Similarity 66.7%;
32; Conservative
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     red. No. 54;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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US-08-774-065-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                           US-08-774-065-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Apr-
                                                                                                                                                                      Best
                                                                                                                                                                                                      Query Match
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-6504 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME Claif of The Content o
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GCTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FABLSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 925 PAGE MILL ROAD CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
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151 ATGAAGTTCCTTCAAGTCCTCCCTGCCCTCATACCGGCCGCCCTGGCC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 43.1%; Score 22.4; E Similarity 66.7%; Pred. No. 54; 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC 48
                                                             1 ATGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC 48
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                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         1050 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1050 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clarkson, Kathle
Larenas, Edmund
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bower, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-846-7620
                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                  43.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/774,065
                                                                                                                                                              Score 22.4;
Pred. No. 54;
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                                                                                                                                                                                                  DB 2;
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Search completed: November 13, 2003, 08:53:19
Job Line: 65 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                    Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using
                                                                                                                                                            000000
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                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                Score
       seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       November 13, 2003, 08:18:16; Search time 216 Seconds (without alignments) 786.790 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2169961 seqs, 1634102185 residues
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_Seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
   6 9 US-09-825-414-37

6 9 US-09-815-242-7958

6 9 US-09-804-5518-43

6 14 US-10-270-333-149

2 14 US-10-270-333-149

5 12 US-10-029-386-713

2 14 US-10-156-761-6808

4 14 US-10-156-761-7129

10 US-09-738-626-337

10 US-09-738-626-337

10 US-09-738-626-337

10 US-10-156-761-2054

10 US-10-156-761-2054

10 US-09-738-626-339

10 US-10-027-632-50396

12 US-10-027-632-50398

12 US-10-027-632-82972
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Sequence 43, Appl
Sequence 149, App
Sequence 148, App
Sequence 7131, Ap
Sequence 7131, Ap
Sequence 7129, Ap
Sequence 1, Appli
Sequence 2054, Ap
Sequence 2054, Ap
Sequence 50396, A
Sequence 50397, A
Sequence 50398, A
                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                          Sequence 7958,
Sequence 43, A
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-128-714-	Ŧ	3-714-	US-10-128-714-7006	-352)-352-1109)-352-4	5-761-	3-995-379	386-81	US-10-029-386-21891	US-09-867-550-223	US-09-878-574-12667	US-10-156-761-1	US-10-267-255-75	US-09-953-348-75	US-10-267-255-83	US-09-953-348-83	US-10-156-761-5574	-10-314-657-	8-846-	-632-8	32.	-10-027-632-8	US-10-027-632-50398	-10-027-632-503	US-10-027-632-50396	-027-632-82	US-10-027-632-82973	
50		e 60	æ	12293	11092	e 476, Ap		Sequence 37972, A	e 8191, A	21891,	N	1266	e 1,	Sequence 75, Appl	e 75,	83,	83, A	55	e 1, Appl	e 12577,	e 82974,	e 82973,	e 82972,	e 50398,	e 50397,	e 50396,	e 8297	73,	

ALIGNMENTS

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FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 37
LENGTH: 336
TYPE: DNA
ORGANISM: Pseudomonas syringae
US-09-825-414-37
RESULT 2
US-09-815-242-7958/c
; Sequence 7958, Application US/09815242
                                                                                                            В
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US-09-825-414-37
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020083489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37,
                                                                                                                                 CAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG
                                                                                                        CTGTTGGCTGGCGCTCTCAACCCCCTTGTGAATGCCGGCCCCGGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09825414
                                                                                                                                                                                  48.1%; ilarity 69.4%; Conservative
                                                                                                                                                                                      0
                                                                                                                                                                                                    Score 25;
Pred. No.
                                                                                                                                                                                  core 25; DB 9;
red. No. 12;
Mismatches 15
                                                                                                                                                                                      15;
                                                                                                                                                                                                                         Length 336;
                                                                                                                                               52
                                                                                                      202
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                                                                                                                                                                                  Gaps
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INFORMATION:

US20020061569A1

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US-09-804-551B-43/c
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                                           US-09-804-551B-43
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/09804551B Patent No. US20020056151A1 GENERAL INFORMATION:
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. :
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7958
  Query Match
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/804,551B
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: DE 100 13 618.4
PRIOR FILING DATE: 2000-03-18
                                                                                                                                                                                                                                                                                                                        APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Receptors for peptides from insects
FILE REFERENCE: Le A 34 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-815-242-7958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert
                                                          NAME/KEY: CDS
LOCATION: (1)..(1563)
                                                                                                                      TYPE: DNA ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                 LENGTH: 1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507 CAGCTCGCTGACCTCCTCGCTCGCCAGCCGGCGACGTCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CAGITCICICACGCICICATCGCICGCICGCCGGCCTCGCCAGIG 52
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Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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    47.3%;
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    Score 24.
    9
    ВП
  9
Length 1566;
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CURRENT APPLICATION NUMBER: US/10/270,333
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/168,677
PRIOR FILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/191,638
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 3772
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ó
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                                                                                   ; ORGANISM: Drosophila
US-10-270-333-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 1566
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/270,333
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/168,677
PRIOR ELING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/175,691
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/191,638
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-270-333-149/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20 GENERAL INFORMATION:
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                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cravchik, Anibal
TITLE OF INVENTION: INCLEDIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
FILE REFERENCE: CL000733CON
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: CL000733CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cravchik, Anibal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 GCACAGCGGTCACGACCTCCTCGCTCCTCGCTGGAGTCCTCCACA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10270333
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    Conservative
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  Score 24.6; D
Pred. No. 16;
O; Mismatches
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Pred. No. 16;
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0; Mismatches
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                                          DB 14;
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    14;
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                                      Length 3772;
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  Indels
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  0
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  Gaps
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6808
LENGTH: 912
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(912)
US-10-156-761-6808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
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US-10-156-761-6808/c
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US-10-029-386-7131/c
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7131
LENGTH: 525
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                                                                                                                                                                                                                                                                                                      APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: ACONTCA-X-2 CURRENT FILING DATE: 2001-12-20
RUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEATURE:

OTHER INFORMATION: MAP TO AL021938.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXTRESSED IN BF311359.1, EVALUE 0.00e+50

OTHER INFORMATION: NT HIT: gi16162622, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1701 GCACAGCGGTCACGACCTCCTCGCTCGCTGGAGTCCTCCACA 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 TGCAGTTCCCTCACAGTCTTCACGTTCTCTTCCCTTGCGAAAGCTCCAGT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
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HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%;
68.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24.4; DB 12;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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RESULT 9
US-10-156-761-1/c
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-282
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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LENGTH: 954
TYPE: DNA
                   SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10156761 Publication No. US20030119018A1
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Publication No. US20030119018A1
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Best Local Similarity
                                                      CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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                                      NUMBER OF SEQ ID NOS: 15109
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LOCATION: (1)..(954)
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LENGTH: 9025608
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HORIKAWA, HIROSHI
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Pred. No. 19;
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; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c,
US-10-156-761-1
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
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US-10-156-761-2054
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 337
LENGTH: 609
Type: 609
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
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Best Local S
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IKEDA, MASATO
OZAKI, AKIO
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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ANDO, SEIKO
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Pred. No. 32;
0; Mismatches
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Pred. No. 14;
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RESULT 13
US-10-027-632-50396/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEC 150 17 NOSC - 7550-08-03
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCCHIAI, KEIKO
APPLICANT: YCKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
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SEQ ID NO 2054
LENGTH: 1455
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
Sequence 50396, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and
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Publication No. US20020197605A1
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Best Local Similarity
Matches 34; Conserv
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Corynebacterium glutamicum
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LOCATION: (1)..(1455)
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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Pred. No. 24;
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and Mapping of Single Nucleotide

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                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50397
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; ORGANISM: Human
US-10-027-632-50396
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 50397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50397, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                          Matches
                                                              Query Match
Best Local (
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LENGTH: 590
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/167,363
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-09-28
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                                                       Similarity
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TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCC 39
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                                          Conservative
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76.3%;
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                                                            76.3%;
                                      Score 23.6; DE Pred. No. 38; 0; Mismatches
                                        0
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Pred. No. 38
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                                                                             DB 12; Length 590;
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FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

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US-10-027-632-50398/c
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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SEQ ID NO 50398
LENGTH: 590
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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   SEQ ID NOS: 325720 FastSEQ for Windows
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76.38;
Version 4.0
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Pred. No. 38;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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US-10-027-632-82974
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; ORGANISM: Human
US-10-027-632-82973
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; ORGANISM: Human
US-10-027-632-82972
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Best Local S
Matches 29
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LENGTH: 590
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82973
LENGTH: 590
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Best Local Similarity
                                     APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20
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29; Conserv
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76.3%;
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Pred. No. 38;
O; Mismatches
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Pred. No. 38;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASISEQ for Windows Version 4.0
RESULT 20
US-10-027-632-50397/c
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US-10-027-632-50396/c
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US-10-027-632-50396
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US-10-027-632-82974
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LENGTH: 590
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                                                                                                                                                                                           Query Match
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 108827.129
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                           264 TGCTGTTTTCTCAAGCCCACAACACTCTCGTCCCTACC
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                                                                                                 2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCC 39
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76.3%;
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76.3%;
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                                                                                                                                                                           Score 23.6;
Pred. No. 3
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Pred. No. 38;
                                                                                                                                                        Mismatches
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                                                                                                                                                                           38;
                                                                                                                                                                                           DB 13;
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Sequence 50397, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

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                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50398
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; ORGANISM: Human
US-10-027-632-50397
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                                                                                                      Query Match
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LENGTH: 590
                                                                  Matches
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/193,483
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
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                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGCTCGCTGCC 39
                                                             l Similarity 76.3
29; Conservative
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76.3%;
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                                                                               45.4%;
76.3%;
                                                             Score 23.6; DB Pred. No. 38; 0; Mismatches
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Pred. No. 3
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                                                                                                    DB 13;
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                                                             Indels
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US-10-027-632-82973
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US-10-027-632-82972
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US-10-027-632-82972
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PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82973
LENGTH: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82973, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 82972
LENGTH: 590
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Pred. No. 3
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSME
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
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US-10-198-846-12577
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US-10-027-632-82974
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                           Sequence 12577, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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ORGANISM: Human
-10-027-632-82974
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 12577
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE: 108827.129
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76.3%;
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76.3%;
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Pred. No. 38;
0; Mismatches
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PREVENTION,
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
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US-10-156-761-5574
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US-10-314-657-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide
TITLE OF INVENTION: Synthases and Methods of Use
FILE REFERENCE: 054030-0021
CURRENT APPLICATION NUMBER: US/10/314,657
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: PCT/US02/08937
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 60/278,935
PRIOR PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 214
SOFTWARE: Patentin version 3.2
SEQ ID NO 1 116630
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                         Sequence 5574, Application US/10156761
Publication No. US20030119018A1
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Best Local Similarity
Matches 29; Conserv
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APPLICANT: CHENG, Yi-Qia
APPLICANT: TANG, Gong-Li
NUMBER OF SEQ ID NOS: 15109
                 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo mapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136
OTHER INFORMATION: n = A,T,C or G
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Pred. No. 32;
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Pred. No. 37;
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APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Waroglu, M
APPLICANT: He, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic ger
FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 1090-03-12
PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR APPLICATION NUMBER: US 08/624,447
PRIOR APPLICATION NUMBER: US 08/624,447
PRIOR FILING DATE: 1996-08-19
PRIOR FILING DATE: 1996-08-19
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US-10-267-255-83
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; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-953-348-83
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Best Local Similarity
Matches 33; Conserv
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LENGTH: 1029
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: PCT/US00/06394
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/266965
PRIOR APPLICATION NUMBER: 09/266965
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 153
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APPLICANT: Mao, Yingqing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1029)
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FILING DATE: 1994-10-06
                  APPLICATION NUMBER: PCT/US94/11279
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30; Conserv
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Sheldon, Paul
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73.2%;
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Pred. No. 43;
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Pred. No. 42
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TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: 600.530US1
CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: PCT/US00/06394
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/266965
PRIOR APPLICATION NUMBER: 09/266965
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: FastSEQ for Windows Version 4.0
SSECTION 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sherman, David. H
APPLICANT: Mao, Yingqing
APPLICANT: Mao, Yingqing
APPLICANT: He, Min
APPLICANT: He, Min
APPLICANT: Sheldon, Paul
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US-10-267-255-75
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                                                                                                                                                                                   Sequence 75, Application US/10267255 Publication No. US20030124689A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.2%;
           APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REFERENCE: 600.455US1
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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PRIOR FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (302)...(302)
OTHER INFORMATION: n is a or t or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Streptomyces lavendulae
FEATURE:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                    11562
APPLICATION NUMBER: US 09/266,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                   9 CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA 49
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Pred. No. 40;
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US-09-878-574-12667/c
; Sequence 12667, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 33; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
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Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
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PRIOR FILING DATE: 1996-08-19
PRIOR APPLICATION NUMBER: PCT/US94/11279
PRIOR FILING DATE: 1994-10-06
PRIOR APPLICATION NUMBER: US 08/133,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (4187715)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces avermitilis
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HORIKAWA, HIROSHI
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Pred. No. 4
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Pred. No. 3
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APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Ath
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US/09/867,550
VUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
TENDOM: 450
                                                                                                                                              ; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: wherein any n is one
US-09-867-550-223
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
ATITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1599-06-14
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Matches
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SEQ ID NO 12667
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                                                                                                           Query Match
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LOCATION: (1)..(271)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
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TYPE: DNA
ORGANISM: Glycine max
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                     13 CACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC
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                                                                       l Similarity 77.8
28; Conservative
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                                                                                       44.6%;
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                                                                       Score 23.2; D
Pred. No. 52;
O; Mismatches
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Pred. No. 53;
0; Mismatches
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RESULT 35 US-10-029-386-21891

Sequence 21891, Application US/10029386 Publication No. US20030194704A1

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US-10-029-386-8191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HOLD HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 88191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                    FEATURE:
FEA
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: HTT: AF282903.1, EVALUE 3.00e-25

OTHER INFORMATION: NT HIT: AF282903.1, EVALUE 0.00e+00
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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TYPE: DNA
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Similarity 70.5%;
31; Conservative
                    CTCTCACGCTCTCATCGCTCGCTGCCGGCCTCGCCAGTG 52
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                                                                                                                                                    44.68;
                                                                                                                      ; Score 23.2; DI
; Pred. No. 52;
0; Mismatches
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Pred. No. 52;
0; Mismatches
                                                                                                                                                                                  DB 12;
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                                                                                                                                                                                  Length 597;
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Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20
                                               S
                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(939)
US-10-156-761-4691
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US-10-156-761-4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-918-995-37972
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US-09-918-995-37972/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
                                                                                                 Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4691, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4691
LENGTH: 939
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis
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LOCATION: (1)...(492)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Local Similarity 68.1%;
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TGCAGTTCTCTCACGCTCTCATCGCTCTCGTTCGCTGCCGGCCTCGCC 48
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ilarity 68.1%;
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Pred. No. 60;
0; Mismatches
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Pred. No. 61;
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Query Match Best Local : Matches

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US-09-960-352-476

US-09-960-352-476

US-09-960-352-476

Sequence 476, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Marten, Wesley C.

APPLICANT: Matchialagan, Nagappan

APPLICANT: Matchialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(1029))C

CURRENT APPLICATION UNMERR: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 476

LENGTH: 322

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 03-BOVMS1-015-Q1-E1-A11

US-09-960-352-476
                                                                                                                                                                                                                                                                     Sequence 11092, Application US/09960352

| Sequence 11092, Application US/09960352
| Patent No. US20020137139A1
| GENERAL INFORMATION:
| APPLICANT: Warren, Wesley C. |
| APPLICANT: Wathislagan, Nagappan OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITLE REFERENCE: 16511.006/37-21(10298)C
| CURRENT APPLICATION NUMBER: US/09/960,352
| CURRENT FILING DATE: 2001-09-24
| NUMBER OF SEQ ID NOS: 15112
| SEQ ID NO 11092
| LENGTH: 379
| TYPE: DNA ORGANISM: Bos taurus OTHER INFORMATION: Clone ID: 48-BOVMS1-002-Q1-E1-D12
| US-09-960-352-11092
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Search completed: November 13, 2003, 09:48:44 Job time: 244 secs
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US-09-960-352-11092
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Matches 30; Conservat
                                                                                      281 TATCGCCCGCTCCTTTCGCTTTCTTCGCTTTCTCGCCA 322
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l Similarity 71.4%;
30; Conservative
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71.4%;
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Pred. No. 73;
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AE005715 Caulobact
AX078430 Sequence
AX305572 Sequence
X05640 Mouse NF-M
                                                                                                                                                                                                                          AR308838 Sequence
AY03793 Phytophth
AY121618 Drosophil
AJ510210 Arabidops
AY05108113 Drosophil
D87440 Human mRNA
BC015052 Homo sapi
AX399923 Sequence
AK074112 Homo sapi
AR7126770 Mycobacte
AR0727055 Human mRNA
U65785 Human mRNA
U65785 Human 150 k
BC033494 Homo sapi
Y08109 G. Sgallus mR
AR206876 Sequence
AR308837 Sequence
AR308837 Sequence
AR308841 Sequence
                                                                                      164799 Sequence 5
X99339 B subtilis
AF318616 Homo sapi
AL157424 Homo sapi
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AX195972
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BD084814 Diagnosis
Y00067 Human gene
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AF064563 Hordeum v
AF145671 Drosophil
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AF039945 Homo sapi
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Direct Submission
Submitted (27-JUL-1995) Texas Center for Infectious Disease, Research Immunology, 2303 S.E. Military Drive, San Antonio, 78223, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
1 (Dases 1 to 1234)
Zhu,Y., Yang,C., Magee,D.M. and Cox,R.A.
Molecular cloning and characterization of Coccid
antigen 2 cDNA
Infect. Immun. 64 (7), 2695-2699 (1996)
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Coccidioides immitis antigen
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Dugger, K.O. and Galgiani, J.N.
Direct Submission
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 1201)
Dugger, K.O., Villareal, K.M., Ngyuen, A., Zimmermann, C.R., Law, J.H. and Galgiani, J.N.
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Coccidioides posadasii
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/translation="MQFSHALIALVA"
/translation="MQFSHALIALVA
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/mol_type="mRNA"
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                  Submitted (12-MAR-1996) Rebecca A. Cox, Clinical Investigation, Texas Center for Infectious Disease, 2303 S.E. Millitary Dr., S Antonio, TX 78223, USA
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 1435)
Zhu,Y., Yang,C., Magee,D.M. and Cox,R.A.
Coccidioides immitis antigen 2: analysis of gene and protein
Gene 181 (1-2), 121-125 (1996)
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Direct Submission
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Coccidioides immitis antigen
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PSETAEPTAEPTAEPTAEPTAEPTAEPTHEPTEEPTAVPTGTGGGVPTGTGSFTVTGR
PTASTFAEFPGAGSNNVASVGGIAAALLGLAAYL"
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/note="21 A nucleotides"
/383 c 277 g 322 t
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Pseudomonas aeruginosa
ĀE004517 AE004091
                                                                                                                                                         Similarity 100. 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUL-1997) Infectious Disease; University of Arizona, 1501 N. Campbell, Tucson, AZ 85724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peng, T., Orsborn, K.I., Orbach, M.J. and Galgiani, J.N.
Proline-rich vaccine candidate antigen of Coccidioides immitis:
conservation among isolates and differential expression with
spherule maturation
J. Infect. Dis. 179 (2), 518-521 (1999)
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Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 3821)
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Location/Qualifiers
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/gene="PRA"
                                                                                                                                                                                                                                                                                                                                             note="antigen 2"
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Pred. No. 2.7e-17;
                                     10822
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FEATURES SOURCE Gene			CONSRTM TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM
Location/Qualifiers 110822 /organism="Pseudomonas aeruginosa PAO1" /mol_type="genomic DNA" /strain==PAO1" /strain==PAO1" /db xref="taxon:208964" 81506 81506 /locus_tag="PAO817" 81506 /locus_tag="PAO817" /note="Protein name confidence: Class 3 (function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene)" /codon_start=1	'Protein name confidence' is used to rate our confidence of the accuracy of the protein name. Class 1: Function experimentally demonstrated in P. aeruginosa. Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known). Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene. Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.	This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada) we welcome submission through www.pseudomonas.com of any proposed changes.		ngt	opportunistic pathogen L Nature 406 (6799), 959-964 (2000) E 20437337 D 10984043 E 2 (bases 1 to 10822) S Stover, C.K., Pham, XQ.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Westbrock Nadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folder, K.R., K.R., Kas, A., Lim, R.M., Smith K.A., Spencer D.H.	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; pseudomonadaceae; Pseudomonas. 1 (bases 1 to 1082) Stover, C.K., Pham, XQ.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F. S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.KS., Wu, Z. and Paulsen, I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an	AE004517.1 GI:9946710 Pseudomonas aeruginosa PAO1 Pseudomonas aeruginosa PAO1
g ene	gene CDS		gene CDS	6	gene gene	gene CDS	
lously rej cously rej protein" l" LLAEPHLTWI LLAEPHLTWI LFDIYGKR VLFDIYGKR JLAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI ALAGGLDAI	/protein id="AAG04209.1" /db_xref="GI:9946714" /tcanslation="MPAVIAENDVSIWDDETGAVYH /translation="MPAVIAENDVSIWDDETGAVYH /translation="MPAVIAENDVSIWDDETGAVYH /translation="MPAVIAENDVSILARAEIKF TDKSFADDRLSAQPHYFGIARIGKVYFDDESILARAEIKF LSTYYGVRYERDPTLRIQAIALHGVACKACGFDFGK APKAVNPETDLVPLCANCHAVVHRRRDRTLSVDELK complement (24643552) /locus_tag="PA0821" /locus_tag="PA0821" /locus_tag="PA0821" /locus_tag="PA0821" /locus_tag="PA0821"	/locus_tag="PA0820" /note="Protein name confidence: Clas previously reported genes of unknown similarity to any previously reporte /codon start=1 /transT_table=11 /product="hypothetical protein"	/protein_id="AAGG4208.1" /db_xref="G1:9946713" /translation="MAPCPGKTVTAQSPSTFIPLRR /translation="MAPCPGKTVTAQSPSTFIPLRR DLFDTARTRLESAIGTLSVLDLLDETEEPGESTCRI 15452357 /locus_tag="PA0820" 15452357	/locus tag="PAO819" /locus tag="PAO819" /note="Protein name confidence: Clas previously reported genes of unknown similarity to any previously reporte /codon start=1 /transT_table=11 /product="hypothetical protein"	ical protein" 1207.1" 712" VYLLLILALTPALASSAT VRKKECATSSLPDEQSSC	/translation="MSLMPFHLAIPVHDLPAARRFY HQLVIHQHPQTDSQRHAGSNPVDGHDVPVPHFGVVL PYIRKGQVGGATLFLFDPCGNALEFKSFRDMGQL complement (\$25 797) /locus tag="PA0818" complement (\$25 797) /locus tag="PA0818"	<pre>/transl_table=11 /product="probable ring-cleaving dio /protein_id="AAG04206.1" /db xref="GI:9946711"</pre>

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DEPSEAFMARMPGLDVGTACLLAN
AQLESSHFAFYRYGDGVVIQAGAYP
GGSHDGELRLVGWAADQWLKRLDVE
                                                                                                                                                                                                                                                                                                                                        NYHYPRRYSAILKPGVQVVYYKGKL
GGDLFALIESFOPFEQAVLAKEGNSY
IIKPLQVAESWGDRALGFESRTEGS
PGKAYGEYAKGFIHVHHTQPISSFE
DELKGLVRGRWVCAEADVVV"
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QLFAK"
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RITGSLLSLFEAEYARRHR"
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AE012448 AE008922
AE012448.1 GI:21114551
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         Xanthomonadaceae; Xanthomonas.
1 (bases 1 to 13170)
                                                          Xanthomonas campestris pv. campestris str. ATCC 33913
Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; Gammaproteobacteria; Xantho
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/locus tag="pA0824"

/locus tag="pA0824"

/note="Protein name confidence: Class 4 (homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences)"

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complement(4037. .4270)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
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SDCDCGQENQRSKVPVEQAGWAVAIAGGVMFVLTRGRSPRPMIPAY"
Complement (4037. .4270)
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asacgspmisavsstvlinglpavtlgsigahgnvviggsgtvligdvftpaprapal
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ILYIDLVQRCDA"
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complement (4000)
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%; Pred. No. 3.4
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RS da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., and Silva,A.C.R., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Chambergo,F., Ciapina,L.P., Ciarelli,R.M.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,B.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Machado,M.A., Manck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
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Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-NOV-2001) Departmento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitted (28-NOV-2001) Departmento de Bioquimica, Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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)3913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="pathovar: campestris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF located using Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Universidade de SP 05508-900,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl tah'
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                                       JOURNAL REFERENCE
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ORGANISM
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ACCESSION
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AF416330/c
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                                                                                                             TITLE
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Best Local :
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AF416330
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DND. DNTVAPVLPDLTAATLLGQIRTLRAPDTIRIALIDAQDGQRTPPARIIGVAHRFL
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                                                                                                                                               100.0%;
                                                                                                                                                                        36.5%;
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   7120
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5
                                                                                                                 Mismatches
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                                                                                                                                                                        Length 13170;
                                                                                                                 Indels
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AF416330

DEFINITION Ruegeria sp. PR1b plasmid pSD20, complete sequence.

ACCESSION AF416330

VERSION AF4163301

VERSION AF4163301

KEYWORDS

SOURCE

ORGANISM Ruegeria sp. PR1b

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;

Rhodobacteraceae; Ruegeria.

REFERENCE 1 (bases 1 to 76093)

TITLE

TOURNAL PROTECTION FOR AF416300.

REFERENCE 1 (bases 1 to 76093)

RUEGERIAN RUEGERIAN

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-AUG-2001) Department of Biology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0322,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                 /transl rat?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAHDLLVACNRETSGDAYRRLREAFERLAGTRITTNITTGGHEVTSGFGLIESWEIVR
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AYMGPTLSPHRQDYTALIGQAGEQVNGIYEADYRDFNRETYARGRETFDATYAAFKRL
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1223. .1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>APPTVSEEAREEARRLMPGMDVHALEADWRAVWARTGAPRLRKPDAAFLGWVRKRAQD</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3022. .4191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTGVWRREELALQQERAAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                               note="putative galatosyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="replication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="RB101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="replication protein RepA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /plasmid="pSD20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:185588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="PR1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Ruegeria sp.
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 76093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              start=1
                                                                                                                                                                                                                                                                                                                                5487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(11451. .12566)
/note="no homolog identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDFDSLQNSYGAGYESRTTKGFWQRILGKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical
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L2776. .13981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="polysaccharide export protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                      product="RB107"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLVWSIFVLVYYSIRDRS"
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GKPDRLDHGNRVNDRMGVFDGONPANENGAÐKNIGÐTVEÐETROÐRVDPGDGRVFOGER GRERNGFGGHVGOAG IKREGOI ÞACVEÐKKTGAÐRGAÐKUGÐG GRERNGFGGHVGOAG IKREGOI ÞACVEÐKKTGAÐRGAÐGHÐGAHÐRERKRGGGGHEÐ ÞÐI ÞPGGA ÞYERRHLSGODRAÐRTÖTGEASMYSÐLGÐLGRGHGGLLRRKKGGGGHEÐ SGEYCVVIRRRAGDTLSKMGMTKKTANA PGQAÐMKQÐVGLSEA TASGOÐTÞAQGKAÐ AEENGFRGGGFEKGGLGFI KAQKLREÐVRAÐEAMTRHLQROLÐEQÐA Y PVAR PATLK RRHWGILVSFYLICVLLVVYYKANA I AEÐDVSTSGFVVRSÐÐATAKSELGGLAÐ LKVAR RHKGILVSFYLICVLLVVYYKANA I AEÐDVSTSGFVVRSÐÐATAKSELGGLAÐ LVGDGTAS BOÐLTAKSELLGGLAÐ LVGDGTAS BOÐLYLAFI OSQEI VEVVEREÐYGLRAHFSAHMPGÐMAFALMPÐATLEÐLT
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PIKAVTRHPFPFFRGDDINFSLANEFNIRTLNGVVSFQDDFTEKESAQTLYLDLR:H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAN05126.1"
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VAFVQNFSELGAAFYSPMRTYSSGMRSRLTFGASMGIKFDTYLVDEVTAVGDKSFRDK
                                                                                                       , translation="MAQHKTLIFHLGDCKTGSTSIOTAFAQERVOLQDASVTYPADLA
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ELYSRYFTGIADELRLISYVRPHAARLLSGYSERTKLGVYDAWNDSMETPVEROXDRK
LFFYQPRFAAMRDAFGDAFQLRPMIPAQLHQGSVVQDFLHHAFGGLPTKLIGDEAANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQHLTI PELKRSALGTAKVAI YFTLRSLLRYHYSTAAVQLMAWQDVMKGPQFFEENI
DMSERRATI KEMSADEAWQP I AQVDLSEHRKGVATWSHRARHYWGLFTLNGHI LPCGG
ASKLVVDINRRALVI RAFGAARVSY I NTNRDKAYTVARDRRRFFTLMWQMAKLTWQFR
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YARADIDDAYAQLKAAREALTQFRTRTRILDPQADIGCARMGVMHLQQQLAEALVEYD
LLRGSGLNSUDPRLKTAEKTIDVIRERIDIERQTFASDNTETGGLGENYESLISEYERL
TVDQQYAEQVYRASLATLEVARDEATRQSRYLATYIKPTLPESSQYPDRPVMAGIAGL
SLCLEDLMRLKVVQRHLTVSADVRHTIGWDIMHKFADMPPANPATKLRLHKSLAKDIR
ATYLEDARALDKTFFGKAPLMERELKAAIKNAADTPQRLEPSDHLAPEELRSLRLLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRVIFAERMKTSSAIMVNHNLNEVRQFCDAGIVLERGRATYFDDLDEAIALHQAMMMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="no homolog identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="putative polysaccharide export protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence similarity;
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JOURNAL
REFERENCE
AUTHORS
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AP005679/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS TITLE
                                                                                                                                                                                              TITLE
JOURNAL
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Best Local
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Oryza satīva (japonica cultivar-group)

Oryza satīva (japonica cultivar-group)

Oryza satīva (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7461)
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                                                                                                                                                                                                                                       Publ
                                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T., Matsumoto,T. and Katayose,Y Oryza sativa nipponbare(GA3) genomic DI clone:OJ1210_A07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
OJ1210_A07, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP005679
AP005679.1 GI:22775437
                                                                                                                                                                                              Submitted (05-SEP-2002) Takuji Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP005679
                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                        Sasaki, T., Matsumoto, T. and Katayose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCGCTGCCGGCCTCGCCA 49029
                                                                                                                                                                                                                                                                                                             olished Only in Database (2002) (bases 1 to 134963)
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GKDLYEAFFKGYTIKQMGVHPSELPASILKRLPVRFNYDDNYFFHKFQGMPENGYTSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MISGSKGESMMTTHADLDSLFQSDWYLEQNPDVADHFVGSALEH
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QVQEKALLADYVKLAEETSGVTFVGRLGTYRYLDMDVTIREALDTARGFEAKTAAGDP
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/product="RB110"
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Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
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Yano, M., Jiang, J. and Gojobori, T.,
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
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NOTE: It currently consists of 1 contigs between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Aug 31, 2001 this sequence version replaced gi:14522861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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                                                                                                                                                   Direct Submission
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Sasaki, T., Matsumoto, T.
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AP003250.3 GI:15
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/mol type="genomic DNA"
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/db xref="taxon:39947"
/chromosome="9"
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complement (join)	gene		misc feature
DQLVDPEIGYETDSET		complement (866010035)	gene
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VHKLARLNNSTGCS I F		/db <pre>/db <pre>/db</pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>	
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similar to wall-		1136 4363 4366 1131	2000
/note="contains		TFFGRFHLPDDAVVDLVRASMDGGMLTVTVPKVVTDKQPAIAAAAPVPAVVAPAVEAK	
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RRPWRPVLVAIPE"		unknown protein"	
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SYRPDYAAAGEEDDGI			
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_			source
IDWKETPESHVFKADI		Location/Qualifiers	
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/dh yraf="GI:15/			anr
/product="pucation"		_	inf
/codon_start=1		JNBa0083M16 and ends at the position 5205 of P0480E02	080
=		REPURED OF this Clone starts at the position 130 000 of	APL
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1362514077	CDS	with OSJNBa008	Thi
	Action	The orientation of the sequence is from T7 to SP6 of the PAC clone.	The
GOTARRES 1363E		classified as a 'hypothetical' protein.	18
Z		dimost the entire length of partial sequence) is classified as an	ur.,
/translation="M		significant homology to any protein but with EST homology (covering	513
/db xref="GI:15"		ch as same name, 'putative-' and '-like protein'. A gene without	ons
/product="putat;		classified based on the protein name to indicate the homology level	cla
/codon_start=1		dene with identity or significant homology to a protein is	A C
		1 the	the
/gene="P0443D08	0	NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent	NCE
/gene="P0443D08	CDS	Protein homologies of the coding regions were searched	RGP.
complement (105	gene	e, nr	NCE
pse		sion). The genomic	(00
gimilar to non-			GEN
יחסר ביי "הפסולסקפו		Genes were predicted from the integrated results of the following:	Ger

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n="MSDSFFFVVVSAWSLALMLAAAARGAEEEGGGCLGSOKCGDLN
n="MSDSFFFVVVSAWSLALMLAAAARGAEEEGGGCLGSOKCGDLN
ADROCGPLDYQVYCNNSTGVATLRSSTDSGFDIINISYGDRTMLVFD
GCSIPVFNTFAKLPITFISPSHINLVFYNCTEAPPAEQQQCLGLVE
GGREFGEGDYDKYYLEGCSRNSTYVFLPULEPPDGKANASRYVELVGG
VTSSAANTAADNRPQEGCAASTVCGKVTISSPAVVPEQATESKCGW
PYLGYYKPRYRIOILDIFYGNNSLLVSDHKLGDEIVFSGVSKEYSC
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TDSETKRMVDLVAELLAFQCLQMDRESRPPIKEVVEVLNCIKMGECPA
DSHLLKDSLLYSPDSVIHRFHSQSTNHSVASNSG"

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GEKSSLLLTSRSSLEELLVSDDADDDGAIDDAAVTCRNASLCAK
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.DLPGVKKEEVKVEVEEGNVLVI SGQRSKEKEDKNDKWHRVERSS
.VDQVKAGMENGVLTVTVPKAEVKKPEVKAI EI SG"
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.VDQVKAGLENGVLTVTVPKAEVKKPEVKAIEISG"
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                                                                                                                                                                                                                                                                   AL Submitted (10-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced.
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Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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2 (bases 1 to 156485)
Sasaki,T., Matsumoto,T. and Katayose,Y.
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/cultivar="Nipponbare"
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                                                                  db_xref="taxon:39947"/chromosome="8"
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
                                                       Oryza sativa (japonica cultivar-group) *** SEQUENCING IN PROGRESS ***.
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Direct Submission
Submitted (11-SEP-2002) Takuji Sasaki, National Institute of
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*** SEQUENCING IN PROGRESS ***.
HTG; HTGS_PHASE2
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AP004776.1 GI:18844996
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasakki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel.81-298-38-7441, Fax:81-298-38-7468)
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/mol type="genomic DNA"
/cullivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="9"
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.

* This sequence will be replaced to by the finished sequence.
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19; Conserv
                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum USDA 110
Bradyrhizobium japonicum USDA 110
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
        Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K.,
                                                                                                           Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110 DNA Res. 9 (6), 189-197 (2002)
                                                                                                                                                                                       Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K., Shanada,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M.
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36993 c 37880 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110 (supplement)
DNA Res. 9 (6), 225-256 (2002)
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Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
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1073. 2126
        /transI tat:
                                                                                                                                                                                                  /translation="mrnalglmlasvvaavvI aaggwfyysasadpgapktvaaraad
plaqotxI aaxddvattaalaakptavagasaptpapvapvogacanpnalgvarv
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VGKHATYHPEILROVLAGCHTVGTHTWSHVNLNSKKWTEQOVKDEVEKGFSAVRFALG
TNPAPFFRFPQLQHNPAMVTYFGTRNVAMFSTDIDSFDFRKGATPEKIVETVMGRLDK
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                                                              /note="ORF_ID:bll0563
hypothetical protein"
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unknown protein"
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\EAQQQCTGDAFRLCSSEIPNIPKITACMMKHRSDLSAGCRAVMDKDLAKGASRKVAD
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EGGG,

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/note="0RF_ID: b110565
hypothetical protein"
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appvsehtepeoakseoadaeperaeaoaavapapasppvspwviaplsgavaaavvi
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/gene="bl10566"
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FASSGI PTPVALSRELLNI VSKLSPPADAQSSGGGI VERLQAGASKLVRI ERTDGVGN
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273395 TCGTCGCTGCCGGCCTCGC 273413
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                                                                                                                                                                                               2 (bases 1 to 1500)
Liolios, K.G., Chu, L.,
Koukharenko, V., Gerdes
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Raymond, J., Zhaxybayeva, O.,
Blankenship, R.E.
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AY142898
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8245. .9225
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GVAANQA1RGALHDVARQAKTQLIMPPPALCTDNGAM1AWAGAERLALGMTDTMEAQP
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9344. .9790
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|db xref="taxon:28064"
|noce="RHM003875"
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                                                                                                                                                                                          hu,L., Ostrovskaya,O., Mendybaeva,N., Gerdes,S., Kyrpides,N. and Overbeek,R.
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                                                                                                                              ics, Integrated Genomics, Inc., IL 60612, USA
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Kluyveromyces yarrowii recombinational repair protein
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72 a 392 c 413 g 323 t
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TVKQQSFMKIFHDLSLSQSLSRHLADFDISTNSLATTSIQIIKDSSKSFSKYCEFS
LIKNIFILREHFIGDFVTQINDVHADFDSRWDBMVVENAGFBYYKCEGRFFTTTHFLV
TNRRAFAIFKHIIDAGSGTLWLCDDISNLDHFIKHITSDNVILLVHLNNGKSSISST
EQSSDLDVQEAKLLKNKAQNLGFRIHDVNDIVQAVLDHNFEKLLERVFVRNLPSKAPT
GPSSDLDVQEAKLLKNKAQNLGFRIHDVNDIVQAVLDHNFEKLLERVFVRNLPSKAPT
GFPLEBATNKSVIKSADTFKPSNKAKRTNRQVVPLDSLAFGGGSAAESKQNFTEVPE
SERGHETSQNTTTTEFABGEFSKAKATIGALRKFDIPNVSEELTEGAINKDKLALVET
SADTSILVQANFKRSKKTLQASEGHTILENDNNSLNIESGPLFKTKSTSLGNEAAQAQ
ADAVQTREAKRFVSFAQAVKETKSHEVDRLEKDIVNVTSEELTEGAINKDNSLNILVET
KDIMBADFFXVGGGGGFGWAGEKKEVTENTURDEGGENEGAINDEGGEN
                        KDLMRADREYAVCGQSGSSEQWAGRKNFKKFVKLWPSRSSRNSPDSATNALRNRAHLI
TREYVPLRPYEGQNANNODDSFLKNSQDDLQEEATCPSIPPVSSTTILGVEVDDEPAF
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/db_xref="GI:30350868"
LFRSQQEDDAYGPDGGLGQRNQHTSVDKDSNRDQELFVFDEEDSQRDHVDTYTDAVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                es St., Cambridge, |
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XRS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:51620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="recombinational repair protein Xrs2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="XRS2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'EC_number="1.1.1.205"
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Pred. No.
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Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                      Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 20, 2000 this sequence version replaced gi:6996979.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence will he preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, Karra, Lee, B., Lewis, S., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Parks, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu.C., and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC009913.10 GI:7264759
HTG; HTGS PHASE1
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished 2 (bases 1
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RPCI-98 04.F.6 map 41C-41C strain y; cn
PROGRESS ***, 41 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC009913
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                                                                             509:
589:
969:
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grap of unknown length of 309 bp in length length of 380 bp in length counting of 380 bp in length gap of unknown length is conting of 527 bp in length counting of 639 bp in length counting of 639 bp in length length gap of unknown length
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42;
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FEATURES

Location/Qualifiers

Score 18; Pred. No.

3200 others

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Mismatches

0; Indels Length 63781;

0

Gaps

0

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8857 Contig
9508 Contig
9508 Contig
10479 Contig
10579 Contig
11287 Contig
11287 Contig
11287 Contig
114722 Gap of
114642 Contig
116361 Gap of
116361 Gap of
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or of 689 bp in length
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of 307 bp in length
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of 643 bp in
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of 571 bp in le
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of 984 bp in
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of 429 bp in
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Contact: sequence_submissions@genome.wi.mit.edu
                               Web site: http://www-seq.wi.mit.edu
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Nusbaum, C. and Lander, E.

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NOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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On Dec 21, 1999 this sequence version replaced gi:6563452
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence will
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g of 716 bp in length

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g of 634 bp in le
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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Drosophila melanogaster BAC library, partial EcoRI in
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/mol_type="genomic DNA"
/strain="y; cn bw sp"
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73062: contig of 614 bp in leng
73142: gap of unknown length
73763: contig of 621 bp in leng
73843: gap of unknown length
74543: contig of 700 bp in leng
74623: gap of unknown length
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5: contig of 219 bp in length
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Bodota, B., Bouck, J., Bowie, S., Brooke, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, S.,
Ouiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Suegang, R.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M.,
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D., and
Glbbs, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 29, 2000 this sequence version replaced gi:6996776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 99277)

1 (bases 1 to 99277)

Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooke, A., Buhay, C., Bunac, C., Brooke, A., Buhay, C., Bunac, C.,
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 14% of reads
Chemistry: Dye-terminator Big Dye: 45% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 69137 bases at least Q40
Consensus quality: 82549 bases at least Q20
Consensus quality: 89824 bases at least Q20
Estimated insert size: 95034; sum-of-contigs estimation
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Rephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophildae; Drosophila.

E 1 (bases 1 to 101579)

E Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,

Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,

Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,

Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and

Rubin, G.M., Farfan, L. L.
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           Direct Submission

Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Aug 2, 1999 this sequence version replaced gi:5649193.

Por further information about this sequence, including its location and relationship to other sequence, please visit our sequence archive web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 56 contigs. The true order of the pieces

is not known and their order in this sequence archive webs.
                                                                                                                                                                                                                                                                                                                                                             Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Madda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L., Brith, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L., Brith, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L., Brith, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L.
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vector_side:right"
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/db_xref="taxon:7227"
/clone="Rep(198-1716"
complement(26106. .26205)
/note="assembly fragment:contig25; vector:Vector_pBACe3.6;
vector_side:left"
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone=lib="RPCI-98 (Roswell Park Cancer Institute
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
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a 20734 c 19813 g 27246 t 4409 others
                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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l. .101579
                                                                                                                                                                                                                                                                                                                                                                                                                                     98885: gap of unknown length
99435: contig of 550 bp in len
99515: gap of unknown length
100107: contig of 592 bp in len
100187: gap of unknown length
100895: contig of 708 bp in len
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Blazej, R.G.,

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Submitted (01-JAN-2003) Seattle Biomedical Research Institution,
Nickerson Street, Seattle, WA 98109-1651, USA
On Jan 12, 2002 this sequence version replaced gi:17017563.
Location/Qualifiers
  Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R.,
                                                                                                                                                                                                                                                                                                             AC009746 123010 bp DNA Drosophila melanogaster chromosome 2 clc RPCI-98 03.D.4 map 40D-40D strain y; cn PROGRESS ***, 80 unordered pieces.
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4 (bases 1 to 117714)
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McDonagh,P., Ivens,A., Nguyen,D., Munden,H. and
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Leishmania
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
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Drosophila melanogaster (fruit fly)
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/mol type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
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chromosome="35"
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On Mar 20, 2000 this sequence version replaced gi:7105464.

On Mar 20, 2000 this sequence version replaced gi:7105464.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 80 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
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Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L.
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84537 contig of 513 bp in length
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85801 gap of unknown length
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87801 contig of 694 bp in length
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Submitted (05-JAN-2002) Seattle Biomedical Research Institution, Nickerson Street, Seattle, WA 98109-1651, USA On Jan 29, 2002 this sequence version replaced gi:18071338.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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124612 bp DNA linear HTG 29-JAN-2002

Leishmania major chromosome 35 clone LB00329 strain Friedlin, ***
SEQUENCING IN PROCRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2.
Leishmania major
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Myler,P.J., Sisk,E., Mack,J., Nelson,S., V.
Myrthey,L., Ivens,A., Marty,A., Munden,H.,
                                                                                                                                                                                                                                                                                                                                          AC105442.2 GI:18390199
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of 378 bp in
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of 264 bp in
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Vogt,C., Robertson,L., ., Stuart,K., Seyler,A.

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E 1 (bases 1 to 127091)
S Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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Submitted (03-SEP-1999) Drosophila Genome Center, Lawrence Berk Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 28, 2000 this sequence version replaced gi:6980150. For further information about this sequence, including its loca and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send em to bdgp@fruitfly.berkeley.edu. All contigs in this submission me following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 93 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                            Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej Butenhef, C., Champe, M., Chavez, C., Chew, M., Classiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L. Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearne Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Peacleb, J.M., Park, S., Ffeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirska, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster chromosome 3 clone RPCI-98 01.6.11 map 80B1-80D2 strain y; cn PROGRESS ***, 93 unordered pieces
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Drosophila melanogaster (fruit fly)
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/db_xref="taxon:5664"

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103780: contig of 103780 bp in length
103930: gap of unknown length
106086: contig of 2156 bp in length
106236: gap of unknown length
124612: contig of 18376 bp in length.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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10: contig of 680 bp in length
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Sequencing of Drosophila chromosome 4, region 1015-1025
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and relationship to other sequences, please visit our se archive Web site (http://www.fruitfly.org/sequence/) or to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                          Submitted (27-SEP-1999) Drosophila Genome Center, Lawrenc Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jan 10, 2002 this sequence version replaced gi:7116216
                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Stirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                        This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                    Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS
Berkeley, CA 94720
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1 (bases 1 to 11784)
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Eukaryota; Metazoa; Arthropoda; Hexapoda;
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4, region 101F-102F, BAC clone
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Direct Submission

AL Submitted (21-DEC-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
On Dec 21, 2002 this sequence version replaced gi:24270659.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are three areas of single-subclone: $4456-54560, 57568-57653 and 115543-115568. From base 133735. There are only PCR reads. The assembly overlaps from 139009-162132 bases on OSJNBa0090010. The assembly overlaps from base 136321-149349 with OJ1263H11 (accession # AC118980). The
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1 (bases 1 to 149349)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T. Collura,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-SEP-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA 3 (bases 1 to 149349) wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T.Currie,J. and Collura,K.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplaniae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                         Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-OCT-2002) Arizona Arizona 303 Forbes, Tucson, AZ
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="101F-102F"
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/db_xref="taxon:7227"
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85721, USA
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Rocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rolt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Feiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Sequencing of Drosophila chromosome 2R, region 41E-41E
AL Unpublished (1998)
DE Colniver S. R. Achamia Accessed T. Barray E. Blazai B.G.
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Arizona
                                                                                                                                                                                                                                                                                                                                          Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M. A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snit, E., Potan, L., Shit, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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                                                                                                                                                                                                   Submitted (17-AUG-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Dec 14, 2001 this sequence version replaced gi:7264782.
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location
                                                                                     Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory,
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                  Direct Submission
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/note="(japonica cultivar-group)"
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/mol_type="genomic DNA"
/db_xref="taxon:39947"
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                                                                                                                                                                                        Agrobiological Resources, Nacional MacLoual Institute of 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL.hhtp://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7460)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This is a 'working draft' sequence.

* This sequence will be replaced to be the finished sequence.

* This sequence will be preserved.
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Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kanno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP003935.1 GI:14915718
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pBACe3.6)"
a 29939 c 31348 g 48335 t
                                                   /mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
                                                                                                                                organism="Oryza sativa
                                                                                                                                                                          Location/Qualifiers
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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5': RP11-486B10 AL445933, 2000-bp
3': RP11-216M14 AL451006, 2370-bp
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                                                                                                                                              Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 160573)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond
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Kaul,R.K., Olson,M.V., Zhou,Y.,
Saenphimmachak,C., Phelps,K.A.,
and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 1 clone RP5-820016, complete sequence AC119676 AL157905 AC119676.2 GI:22024581
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Haugen, E.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                   This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality
           Base-by-base quality values are not generally visible GenBank flat file format but are available as part
                                                                        Quality levels above 40 are expected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fomo sapiens (human)
                                                      l error in 10,000 bp.
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                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 69% of reads sequencing vector: plasmid; L08752; 31% of reads Chemistry: Dye-terminator Big Dye, Assembly program: Phrap; version 0.990319 Consensus quality: 160468 bases at least Q40 Consensus quality: 160565 bases at least Q30 Consensus quality: 160573 bases at least Q20 Insert size: 160573; sum-of-contigs Quality coverage: 8.7x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: chr-1
Center clone name: RP5-820016 (sc0838)
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: uwgchtgs@u.washington.
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: University of Washington Genome Center Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genome.washington.edu
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entry's ASN.1 file.
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Pred. No.
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Buckley,D.,
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Kibukawa,M., Raymond,C.
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Kibukawa, M., Raymond, C.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear

	272	6606		<800	
1963	198	3950	u	3625	
5015	52	<800	• • • •	1482	: 1
~800	571	<800	! !	1846	1
3122	309	<800		3237	1
6701	668	11922	119	4729	:
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<800	79	996	:	2155	
2947	292	4743		<800	; ; ;
1438	145	<800	•	937	1 1 1
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4059	409	<800	48	1047	: 1
3629	357	1161	117	3434	:
2947	! !	3280	326	3434	. ω
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5218	5062	<800	4.8	2828	281
7290	727	7987	806	<800	512
5578	567	2124	2	<800	, , , ,
8725	887	3280	3216	4729	4651
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34.6%; 100.0%;	Location/Qualifier 1160573 /organism="Homo sa	<800	2155	2828	14543	19745	<800	2155	1846	1653	4315	1223	<800	11253	<800	6779	1846	2828	2828	7061	13799	<800	7498	<800	1653	<800	4729	2506	3434	1223	781	1223
Score 18; DB Pred. No. 36;	ifiers mo sapiens"				353	302	720	173	52		327	210	6645	627	6018	764	100	950	29	627	125	178	93	77	325	129	237			603	720	6623
9;	-			1472	3528	3076	7242	1737	<800	828	3280	2124	6606	6300	5928	7642	996	9445	<800	6300	1256	1737	996	760	3280	1256	2367	9188	2941	5928	7242	6606
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																		4699	5015	1028	9559	2497	2069	<800	4233	1219	11239	8296	5578	15722	11239	1722

	TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	RESULT 30 AC012389 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS
569: contig of 569 bp in length 570 649: gap of unknown length 650 928: contig of 279 bp in length 929 1008: gap of unknown length 1009 1403: contig of 395 bp in length 1404 1403: gap of unknown length 1404 12103: contig of 620 bp in length 2104 2183: gap of unknown length 2104 2183: gap of unknown length 2184 2781: contig of 660 bp in length 2782 2661: gap of unknown length 3523 3602: gap of unknown length 4273 3603 4192: contig of 661 bp in length 4273 4272: gap of unknown length 4273 4898: contig of 626 bp in length 4273 4898: contig of 626 bp in length 4899 4978: gap of unknown length 5330 5409: gap of unknown length	Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M. Direct Submission Submitted (27-OCT-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 24, 2000 this sequence version replaced gi:6996991. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet * NOTE: This is a 'working draff' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence secred.	Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster Unpublished 2 (bases 1 to 161518) Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacle, B., Mazda, P., Moshrefi, R., Moshrefi, M., Nixon, K., Pacle, J.M., Park, S., Preiffer, R., Park, S., Pack, S., Park, P	143869 GCAGTTCTCCCACGCTCT 143886 30 9
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Klein,J., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwnan,K., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., McEwnan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:6984402.
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1 (bases 1 to 173093)
Birren, B., Linton, L.,
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AC013579.4 GI:7229999
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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2770
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1447: gap of
2769: contig
2869: gap of
4168: gap of
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6650: gap of
8819: contig
8919: gap of
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f 100 bp
g of 12891 bp
f 100 bp
f 160 bp
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f 100 bp
g of 7625 bp :
f 100 bp
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f 100 bp
g of 8188 bp
f 100 bp
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f 100 bp
g of 4046 bp i
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100 bp
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ISM Drosphila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

CE 1 (bases 1 to 173874)

RS Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

RS Adams, M.D., Celniker, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X.,

Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,

Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor, G.L.,

Abril, J.F., Agbayani, A., An, H.J., Andrewa-Pfannkoch, C., Baldwin, D.,

Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M.,

Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S.,

Burtis, K.C., Busam, D.A., Butler, H., Cadleu, E., Center, P.,

Burtis, K.C., Busam, D.A., Cawley, S., Dahlke, C., Davenport, L.B.,

Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B.,

Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C.,

Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S.,

Geibart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
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154950. .173093
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83873. .93356
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118469. .135438
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105478. .118368
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100.0%; Pred. No. 36;
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JOURNAL
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AUTHORS
TITLE
                                                                                                                                                                        COMMENT
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RS Celniker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., RS Celniker, S.E., Adams, M.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Barans, C.A., Gocayne, J.D., Banzon, J., Beeson, K.Y., Busam, D.A., Crison, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferrisera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Logora, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M., Seguencing of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N. V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Sanders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, B.C., Siden-Kiamos, I., Stapleton, M., Skrong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Welson, M., Weissenbach, J., Walliams, S.M., Woodaget, Wooley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zhong, W., Zhong, W., Zhou, X., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.
The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., Celniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., d. Grey, A.D. N.J., Harris, N.L., Kronmiller, B., Marshall, B., Milburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E., Shu, S., Smutniak, F., Whitfield, B.J., Ashburner, M., Gelbart, W.M., Rubin, G.M., Mungall, C.J. and Lewis, S.E. Annotation of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-SEP-2002) University of California Berkeley, Sciences Addition, Berkeley, CA 94720, USA 6 (bases 1 to 173874)
                                                                                                                                                            Submitted (23-JAN-2003) University of California Berkeley, Sciences Addition, Berkeley, CA 94720, USA On Feb 14, 2003 this sequence version replaced gi:22759414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (bases 1 to 173874)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
5 (bases 1 to 173874)
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       /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                                        replaced gi:22759414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (17702. .18272)
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complement (17702. .18272)
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/product="CG32013-pA"
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/db_x
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complement(13288. .13761)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="CG32013"
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/db_xref="FLYBASE:PBgn0052013"
complement(join(22335. .22528,22617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (11691 . . 12255)
/map="102A1-102A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:FBt10020401" complement (22335. .23205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (13288.
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/map="102A1-102A1"
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                                                                  /locus_tag="CG17923"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join (22335. . 22528, 22617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="CG32013"
/note="last curated on Thu
/map="102A1-102A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transposon="1360{}1476"
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/db_xref="FLYBASE:FBti0020399"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transposon="GATE{}1474"
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/db_xref="FLYBASE:FBt10020395"
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complement(638. .1719)
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/chromosome="4"
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.25153,25218. .25450,25501. .25621)
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                                                                                                             25 15:33:46 PDT 2002"
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TITLE
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AUTHORS
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AC007587
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KEYWORDS
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Best Local (
                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CE 1 (bases 1 to 185916)

CE 1 (bases 1 to 185916)

RRS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Dayle, C., Dresnek, D., Farfan, D., Carlson, M., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R. F., Garg, N. S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Mocintosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Unpublished (1998)

CE 2 (bases 1 to 185916)
2 (bases 1 to 185916)
2 (bases 1 to 185916)
2 (clniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lonotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M.M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185916 bp DNA linear INV Drosophila melanogaster, chromosome 2R, region 41C-41D, BACR02D22, complete sequence.
AC007587
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Drosophila melanogaster
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NVEDLEDGYGOEMTYREEKVLEYTAGTGFFVSIVVTQVFDLLICKTRRNSILQOGMGN
NVEDLEDGYGOEMTYREEKVLEYTAGTGFFVSIVFT
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complement(}0in(26482. .26667,27167. .27349,28371.
28966. .29301,29356. .30391,30551. .31625,31703. .
33949. .34110)}
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/note="CG17923 gene_product"
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/locus_tag="CG32011"
/note="last curated on Thu Aug
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Drosophila melanogaster chromosome 2 cl
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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Submitted (19-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Dec 14, 2001 this sequence version replaced gi:7264774.
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1 (bases 1 to 187223)
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Berkeley, CA 94720
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham, I Anderson,S., Baldwin,J., Barna,N., Bastlen,V., Bedd,F Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett, G., Boguslavkiy,L., Control of the control of th
   Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2: gap of unknown length
6: contig of 694 bp in length
2: contig of 694 bp in length
2: contig of 446 bp in length
2: gap of unknown length
2: gap of unknown length
6: contig of 324 bp in length
6: gap of unknown length
6: gap of unknown length
3: contig of 1317 bp in length
3: contig of 575 bp in length
8: contig of 575 bp in length
8: gap of unknown length
8: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:6759157.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoyle, C.M., Farfan, D.E., Galle, R., Ling, H., Moshrefi, A.R., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, A.R., Noshrefi, A.R., Noshre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukarycta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

E 1 (bases 1 to 189893)

Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L., Hinkle, A., Hoskins, R. A., Houston, K. A., Hummasti, S. R., Karra K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A. R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R. R., Wan, K. H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G. M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189893 bp DNA linear HTG 17-MAR-2000 Drosophila melanogaster chromosome 2 clone BACR25010 (D1173) RRCI-98 25.0.10 map 400-40D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 184 unordered pieces.

AC013254
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Drosophila melanogaster
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103818: contig of 4 101818: gap of unkn 101818: gap of unkn 109 104685: contig of 7 1066 104765: gap of unkn 10537: contig of 8 105717: gap of unkn 106017: contig of 3 106097: gap of unkn	99336 99914 CONTINE 99915 99994 gap of 99995 100377: CONTINE 99995 100377: CONTINE 00378 100457: gap of 010458 101024: gap of 01025 101605: CONTINE 01606 101685: gap of 01606 102540: CONTINE 01607 103304: CONTINE 013305 103304: Gap of	34 53639: contig of 3006 to 53719: gap of unknown 1 20 55306: contig of 1587 to 755386: gap of unknown 1 87 61387: contig of 6001 to 6	34 3653: gap of unknown length 38 3874: contrig of 1641 bp in 75 38354: gap of unknown length 75 39889: contrig of 1535 bp in 76 39889: contrig of 1762 bp in 77 41731: contrig of 1762 bp in 78 41811: gap of unknown length 79 41821: contrig of 2018 bp in 79 43829: contrig of 2725 bp in 79 43829: gap of unknown length 70 43829: gap of unknown length 71 48634: contrig of 2725 bp in 72 48555: contrig of 1851 bp in 73 48744: gap of unknown length 74 48645: gap of unknown length 75 48565: contrig of 1908 bp in 75 48563: gap of unknown length	of 1133 b unknown 1 of 394 bp of 394 bp of 1134 b 1134 b unknown 1 of 1136 b unknown 1 of 1840 bp unknown 1 of 1840 b unknown 1 of 1340 b unknown 1 of 1340 b

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* NOTE: This is a 'working draft' sequence. It currently consists of 184 contigs in the submission meet sis not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence will he reserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, I., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Ji, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, Ji, P., Ling, H., Moshrefi, R., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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109478: contig of 736 bp in length
109558: gap of unknown length
110172: contig of 614 bp in length
110252: gap of unknown length
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                                                                                                                                                                                                                                                                   AL Submitted (28.APR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 17, 2000 this sequence version replaced gi:7159347.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 103 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence so see as soon as it is available and the accession number will
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster
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198282 bp DNA linear HTG 17-MAR-2000 Drosophila melanogaster chromosome 2 clone BACR05A24 (D603) RPCJ-98 05.A.24 map 41C-41D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
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2: contig of 479 bp in length
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3: contig of 463 bp in length
3: gap of unknown length
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38	34.6%; Score 18; DB 2; Length 198282; 100.0%; Pred. No. 36; htive 0; Mismatches 0; Indels 0;	gap of unknown lengt	gap of unknown lengt	conti		gap of unknown	gap of unknow	contig of 712	contig of 1027 b	gap of unknow	gap of unknown lengt	conti	contic	gap of	gap of unknown lengt	contig	conti	gap of unknown lengt	gap of unknown length	conti	gap of	gap	COD	167263: contig of 1000 bp in length	gap	gap	con	Con	con	gap	gap of	gap o	contig of 579	contig of 719	gap of	gap of unknow		contig of 243 k	gap of	gap of unknown	contig of 481 k	contig of	gap of unknown	gap of unknown	unknown of 1296	

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	COMMENT	TITLE JOURNAL	TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS	Db 93843 RESULT 39 ACCOS ALOCUS DEFINITION D ACCESSION AVERSION KEYWORDS SOURCE ORGANISM E
archive Web site (http://www.fruitfly.org/sequence) archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. **NOTE: This is a 'working draft' sequence. It currently consists of 103 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. **P27 1006: gap of unknown length 1302 1381: gap of unknown length 1302 1381: gap of unknown length 1302 1381: gap of unknown length 1403: contig of 495 bp in length 1403: contig of 479 bp in length 1589: gap of unknown length 15975: gap of unknown length 15976 1598: gap of unknown length 1599: gap of	Laboratory, MS 64-121, Berkeley, CA 94720, USA On Mar 17, 2000 this sequence version replaced gi:7159347. For further information about this sequence, including its location	Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M. Direct Submission Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley	Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster Unpublished (bases 1 to 198282) Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Dyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Mediffer, A., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,	, ; ;	
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contig of 1086 bp in
gap of unknown length
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ig of 1027 bp in length
of unknown length
ig of 712 bp in length
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ig of 1083 bp in length
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g of 449 bp in length
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g of 301 bp in le
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Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 15, 2002 this sequence version replaced gi:7259652.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdggefruitfly berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 136 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Feutenboff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, F., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Direct Submission
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, I Gelniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, I Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, I Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Mobhrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 201451)
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AC013831
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Drosophila melanogaster (fruit fly)
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be preserved.
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era; Muscomorpha;
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Human RNA-associat
Drosophila melanog
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S. rochei strain E
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Drosophila mela
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Human cDNA differe
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Human RalGDS (hRal
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Drosophila melanog
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AAD50522/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a partial genomic clone zmGRP3 encoding maize glycine-rich protein 3 (GRP3). This sequence comprises 5' and 3' regulatory elements useful for cloning and expressing root specific or root abundant genes in plants, especially monocots which provide high expression efficiency and high tissue specificity. Root preferred gene expression provides several advantages to plants e.g. resistance to pathogens, pests, herbicides and adverse weather conditions, modification of growth rate and alteration root tissue function. This sequence also provides a means of isolating related regulatory sequences of other plant species which confer root specificity to genes of interest operably linked to them.
                                                                                                                                                                                                                                 Mycobacterial sulphation pathway; immune response; infection; vgene therapy; glycosyl sulfotransferase; enzyme; AST4 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid sequence is used for cloning specific or root abundant gene in a plant
 19-APR-2002; 2002WO-US12374
                                  31-OCT-2002
                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                                                                                                    Mycobacterium avium AST4 (mav_144) glycosyl sulfotransferase
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19; Conservative
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/*tag= d

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2692..2696

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                                                                                                                                                           Location/Qualifiers
                                                                                                      /*tag=  a
/product= "AST4 protein"
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Pred. No.
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0.62;
                                                                                                                                                                                                                                                    response; infection; vaccine;
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RESULT 3
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Best Local S
Matches 17
    Claim 1;
                                                                     New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to mycobacterial sulphation pathway enzymes and polynucleotides encoding such proteins. Sequences of the invention are useful in in vitro cell-free assay for identifying agents that reduce the activity of the proteins. They are useful for increasing an immune response to pathogenic mycobacterium in a host. They are also useful for creating mycobacterial infection in mammals. Sulphation pathway proteins are useful for reducing the viability and virulence of a mycobacterium. They are used as vaccines and in gene therapy. The present sequence is Mycobacterium avium AST4 (mav_144) glycosyl sulfotransferase DNA.
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P-PSDB;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene;
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26-OCT-2001; 2001US-345953P.
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DB; AAE32776.
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                                                                  detection reagent for detecting for elucidating cell signalling
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Pred. No.
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Sequence Listing; English
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RESULT 4
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                                                                                                                                                                New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL015140-ABL30513).
                                                                                                                                 Claim 1; SEQ ID NO 40832; 21pp + Sequence Listing; English
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P-PSDB; ABB71347.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID
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17; Conserv
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Pred. No.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins

is

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.

MIPO

sequences (ABL01840 (ABB57737-ABB72072)

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RESULT 5
AAA31959
  RESULT 6
AAA31675
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                                                                                                                                                                                            and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonuclectide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are
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                                                                                                                                                         Sequence 276 BP;
                                                                                                                                                                                                                                                                                                                             Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant microsatellite marker #920.
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16; Conserv
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                                                                              CATCGCTCTCGTCGCT 36
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                                                     CATCGCTCTCGTCGCT 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105307
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                                                                                                                                                         60 A; 82 C;
                                                                                                                                                                                  specific economically useful genes
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tive 0;
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Pred. No.
                                                                                                                    Score 16;
Pred. No.
                                                                                                                                                         88 G; 46 T; 0 other;
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                                                                                                        Mismatches
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Best Local S
Matches 16
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                   Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant microsatellite sequence; core repeat sequence; detection; pro DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                    05-JUL-2000
                                                                                                                                                                                                                                                                                                                            Sequence 357 BP;
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                                                                           Plant microsatellite marker #666.
                                                                                                                                                     AAA31705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant microsatellite markers and detection of polymorphic genetic
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                                                                                                                                                                                                                                                                          16;
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FLETCHER CHALLENGE FORESTS LTD
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                                                                                                                                                       standard; DNA; 438
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grandis
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                                 Drmanac RT,
                                                                                                                                        31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                       11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #19966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful to locate specific economically useful genes in plant genomes
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                                                                                   (HYSE-) HYSEQ INC.
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CC Note: The sequence data for this patent did not appear in the printed care for wino intrinvival and not appear in the printed content for a since into the invention.
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Best Local S
Matches 16
                          25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                  25-FEB-2000;
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                             99US-0126264.
99US-0126785.
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Matches 16
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21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Claim 1; SEQ ID No
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23-AUG-2000; 2000US-0649167.
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14-OCT-1999;
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supplement; medical imaging; diagnostic; genetic disorder; ss.
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4818; 103pp; English
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
Matches 16; Conserv
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                                 30-JUN-2000; 2000US-215446P.
                                                                   02-JUL-2001; 2001WO-US20999
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(ZYMO ) ZYMOGENETICS INC
                                                                                                     10-JAN-2002
                                                                                                                                   WO200202604-A2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide comprising leucine-rich repeat proteins 21rr7, 21rr8, 21rr9 and spliced variants of 21rr8, 21rr9. 21rr7, 21rr8, and 21rr9 proteins are useful in directing the secretion of proteins of interest from a host cell and to monitor the secretion of proteins in general from cells and tissues. The 21rr DNA and proteins are useful in diagnosing and treating disorders related to abnormal cell growth including retinoblastoma, renal cell adenocarcinoma, endometrial adenocarcinoma, glioblastoma, neuroblastoma, B-cell lymphotic leukaemia, kidney tumours, germ cell tumours, lung large cell carcinoma, mammary, kidney tumours, germ cell tumours, lung large cell carcinoma, mammary, kidney tumours, germ cell tumours.
                                                                                                                                                                                                                                      Human; secreted protein; immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; gene therapy; immune disorder; hyperproliferative; cardiovascular; angiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon adenocarcinoma, genitourinary tract transitional cell tumours, rhabdomyosarcoma, lung tumour, bladder tumour, oesophagus, pancreas and prostate adenocarcinoma. ZIrr protein is useful for identifying agonists and antagonists of the polypeptide, for drug design, to screen for cell metabolism effecting receptors, for analysis of cell phenotype, and as animal feed supplement and cell culture components. ZIrr DNA is also useful in gene therapy. The present sequence is human ZIrr8 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..cw reucine-rich repeat proteins and polynucleotides, useful for diagnosing and treating disorders related to abnormal cell growth retinoblastoma, renal cell, endometrial adenocarcinoma, leukemia, kidney and lung tumors -
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                                                                                                                                                              WO200112776-A2
                                                                                                                                                                                               Homo
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                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                               15-AUG-2000; 2000WO-US22350
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                                                                                                                                                                                                                              infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetic retinopathy; severe combined immunodeficiency; pancreatitis; rheumatoid arthritis; colorectal adenoma; haemolytic anaemia; cancer; reperfusion injury; arteriosclerosis; wound healing; transgenic anima gene therapy; neoplasm; transgenic; psoriasis; ischaemia; carcinoma;
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P-PSDB; AAB70072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; atherosclerosis; Alzheimer's disease; LP220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human LP220 secreted protein encoding cDNA.
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215..2071
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167..2074
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Pred. No.
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26;
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14-SEP-2001; 2001WO-US26026

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RESULT 14
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Best Local (
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                                                                                                                                                                     Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; gene; cell proliferation; haematopoiesis; wound healing; angiogenesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psoriasis, diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury
        08-MAR-2001; 2001US-274101P
                                         08-MAR-2002; 2002WO-US07288
                                                                             19-SEP-2002
                                                                                                             WO200272771-A2
                                                                                                                                                                                                                                                                                                                                                                     Human NOV44b coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV99421 standard; DNA; 2451 BP
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12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
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WPI; 2002-732824/79
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98 - MAR - 2001 | 2001US - 274194 P.
99 08 - MAR - 2001 | 2001US - 274391 P.
90 09 - MAR - 2001 | 2001US - 274391 P.
91 13 - MAR - 2001 | 2001US - 275579 P.
91 13 - MAR - 2001 | 2001US - 275579 P.
92 13 - MAR - 2001 | 2001US - 275601 P.
93 14 - MAR - 2001 | 2001US - 275601 P.
94 15 - MAR - 2001 | 2001US - 275601 P.
95 16 - MAR - 2001 | 2001US - 27599 P.
96 20 - MAR - 2001 | 2001US - 27732 P.
97 20 - MAR - 2001 | 2001US - 27732 P.
98 21 - MAR - 2001 | 2001US - 27732 P.
98 22 - MAR - 2001 | 2001US - 27732 P.
99 22 - MAR - 2001 | 2001US - 27733 P.
99 23 - MAR - 2001 | 2001US - 27733 P.
99 24 - MAR - 2001 | 2001US - 27733 P.
90 25 - MAR - 2001 | 2001US - 27733 P.
91 27 - MAR - 2001 | 2001US - 27793 P.
92 27 - MAR - 2001 | 2001US - 27993 P.
93 - MAR - 2001 | 2001US - 27993 P.
94 27 - MAR - 2001 | 2001US - 27993 P.
95 28 - MAR - 2001 | 2001US - 27993 P.
96 29 - MAR - 2001 | 2001US - 27993 P.
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94 31 - MAY - 2001 | 2001US - 28099 P.
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96 31 - MAY - 20
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Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ; Boldog FL, Li L, Zerhusen BD, Tchernev VT, Gangolli EA; Vernet CAM, Pena CEA, Burgess CE, Liu X, Sprtek KA, Gorman L; Spaderna SK, Voss EZ, Malyankar UM, Anderson DW, Patturajan M; Miller CE, Taupier RJ, Padigaru M, Shenoy SG, Kekuda R, Gusev VY; Pochart PF, Zhong M;

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RESULT 15
ABV99422
ID ABV99
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AC ABV99
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Best Local S
Matches 16
                                                                                                                                                                                             Human; anti-HIV; cytostatic; antidiabetic; antiasthmatic; cachexia; AIDS; antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVx, NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; call differentiation; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
     08-MAR-2001; 2001US-274101P.
08-MAR-2001; 2001US-274194P.
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                                                                        08-MAR-2002; 2002WO-US07288.
                                                                                                    19-SEP-2002
                                                                                                                                                                                                                                                                                                                                     Human NOV44c coding sequence.
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                                                                                                                                                        sapiens
                                                                                                                                                                                    proliferation; haematopoiesis;
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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    New NOVX polypeptides and polynucleotides, useful for preventing
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Spaderna SK,
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16-MAR-
P-PSDB; ABP70144.
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10g FL, Li L, Zerhusen BD, Tchernn

et CAM, Pena CEA, Burgess CE, Lit

erna SK, Voss EZ, Malyankar UM, J

er CE, Taupier RJ, Padigaru M, St

art PF, Zhong M;
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                                                                                Smithson G, Guo X, Gerlach V, Casman usen BD, Tchernev VT, Gangolli EA; Burgess CE, Liu X, Spytek KA, Gorman Malyankar UM, Anderson DW, Patturajan Padigaru M, Shenoy SG, Kekuda R, Gus
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RESULT 16
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                                                                                                                                                            paralysis;
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                                                                                                                                                                    CC 1250 residue amino acid sequences, given in the specification, or a biologically active or immunogenic fragment of the isolated polypeptide is useful for screening a compound for CC The isolated polypeptide is useful for screening a compound for CC effectiveness as an agonist or antagonist of the isolated polypeptide. CC The isolated polypeptide is also useful as an immunogen for preparing CC polyclonal or monoclonal antibodies by hybridoma technology. The CC disolated polypeptide and its encoding polynucleotide are useful for CC diagnosis, treatment and prevention of cancer, actinic keratosis, cc arteriosclerosis, attherosclerosis, bursitis, citrihosis, hepatitis, CC arteriosclerosis, attherosclerosis, bursitis, ctron's disease, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic callergies, anaemia, autoimmune thyroiditis, Crohn's disease, atopic collectis, disease, disease, glamerulonephritis, cc rheumatoid arthritis, scleroderma, systemic lupus erythematosus, cc rheumatoid arthritis, scleroderma, systemic lupus erythematosus, cc rheumatoid arthritis, scleroderma, systemic lupus erythematosus, cc systemic sclerosis, uccertail, fungal, parasitic, protozoal, helminthic infections, trauma, cc allersis, epilepsy, stroke, Huntington's disease, multiple sclerosis, conteriodus extrapyramidal disorder, motor neuron disorder, and conterder averder and conterder and conterders, metabolic, endocrine and toxic myopathies, contribudic naralogis, mentabolic, endocrine and toxic myopathies, contribudic naralogis, mentabolic, endocrine and toxic myopathies, contribudic naralogis, and conterders and conterders, metabolic, endocrine and toxic myopathies, conterders and conterders.
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Thangavelu K,
Honchell CD,
Ramkumar J, M
Kamigaki LL,
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                           periodic paralysis, mental disorders including mood, anxiety and schizophrenic disorders, anaemia, renal tubular acidosis, epilepsy, hypothyroidism, glaucoma, sensorineural hearing loss and cataract. This polynucleotide sequence represents the DNA encoding a human MDDT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel molecules for disease detection and treatment and polynucleotide encoding them useful for diagnosing, preventing or treating cell proliferative, autoimmune/inflammatory, neurological and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001; 2001US-295257P

08-JUN-2001; 2001US-297220P

21-JUN-2001; 2001US-300526P

29-JUN-2001; 2001US-301874P

22-FEB-2002; 2002US-359413P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide chosen from molecules for disease detection and treatment (MDDT), comprising a one of 39 114-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 128; Page 255; 260pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
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                                                                               16; Conserv
                                     CGCTGCCGGCCTCGCC
                                                                                                                                                                    2569
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mason PM, Z,
Barroso I,
                                                                                                                                                                    ВP;
                                                                                                                                                               361 A; 928 C; 818
                                                                                                 100.0%;
                                                                                                                       30.8%;
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                                                                                                   Score 16; Pred. No
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                                                                                                                   Length 2569;
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                                                                             0,
                                                                           Gaps
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RESULT

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Human; anti-HIV; cytostatic; antidiabetic; antiastnmatic, continuity antiinflammatory; cardiant; haemostatic; neuroprotective; anorectic; nootropic; immunosuppressive; osteopathic; antiparkinsonian; cancer; antiinfertility; cerebroprotective; gene therapy; NOVX; NOV; fertility; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; cardiovascular disorder; bronchial asthma; dyslipidemia; metabolic disturbance; neurogenesis; metabolic syndrome X; wasting disorder; cell differentiation; haematopoiesis single nucleotide polymorphism; SNP; cell proliferation; haematopoiesis county healing; angiogenesis; gene; ds.
08-WAR-2001
08-MAR-2001
08-MAR-2001
08-MAR-2001
09-MAR-2001
12-MAR-2001
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13-MAR-2001
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27-MAR-2001
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29-MAR-2001
20-APR-2001
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2001US-274281P

2001US-27432PP

2001US-275578P

2001US-275579P

2001US-275579P

2001US-275601P

2001US-2767000P

2001US-2767094P

2001US-277321P

2001US-277321P

2001US-27732P

2001US-27732P

2001US-27733P

2001US-27733P

2001US-27783P

2001US-27783P

2001US-27783P

2001US-27783P

2001US-27783P

2001US-27783P

2001US-27899P

2001US-27899P

2001US-27899P

2001US-27934P

2001US-27934P

2001US-280802P

2001US-280802P

2001US-280802P

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2001US-280802P

2001US-280802P

2001US-280802P
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2001US-274194P
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replace(1489,C)
/*tag= d
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/*tag= b
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replace(1123,A)
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard_name=
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30-APR-2001;
02-MAY-2001;
03-MAY-2001;
15-MAY-2001;
16-MAY-2001;
16-MAY-2001;
11-MAY-2001;
11-MAY-2001;
11-JUN-2001;
11-JU
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2001US-2880666P.
2001US-2880528P.
2001US-288528P.
2001US-291190P.
2001US-291240P.
2001US-294489P.
2001US-29489P.
2001US-29489P.
2001US-299303P.
2001US-309344P.
2001US-312903P.
2001US-312903P.
2001US-312903P.
2001US-312903P.
2001US-312903P.
2001US-313331P.
2001US-332772P.
2001US-337726P.
2001US-337726P.
2001US-337726P.
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Spaderna SK, Miller CE, Pochart PF, Rastelli L, Boldog FL, Vernet CAM, WPI; 200 P-PSDB; New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer, Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic 2002-732824/79. DB; ABP70142. FL, Li L, Zerhu
CAM, Pena CEA,
a SK, Voss EZ,
CE, Taupier RJ,
PF, Zhong M; ŗ, Mezes PD, Smithson Zerhusen BD, Smithson G, Guo X, Gerlach V, Casman SJ usen BD, Tchernev VT, Gangolli EA; Burgess CE, Liu X, Spytek KA, Gorman L; Malyankar UM, Anderson DW, Patturajan M; Padigaru M, Shenoy SG, Kekuda R, Gusev ; US Ş

Claim 16; Page 261-262; 619pp; English.

and asthma

The present invention relates to new isolated proteins (NOVX) and their coding sequences (ABY99327-ABY99595 and ABP70149), where X is CC any number from 1 to 48. The NOVX proteins and coding sequences are CC useful in the manufacture of a medicament for treating a syndrome CC associated with a human disease, preferably a NOVX-associated disorder. CC The NOVX coding sequences and proteins are useful for treating, diabetes, cosesity, infectious diseases such as metabolic disorders, diabetes, CC obesity, infectious disease, anorexia, cancer-associated cachexia, CC disease, immune disorders, haematopoletic disorders, cardiovascular CC disease, immune disorders, haematopoletic disorders, cardiovascular CC disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic disorders, fertility, mornic diseases or various cancers. The NOVX coding sequences and proteins may also be used as targets for the CC cidentification of small molecules that modulate or inhibit e.g. cartification, haematopoiesis, cell differentiation, cell proliferation, haematopoiesis, contended in the chargey, in generation of wound healing and angiogenesis, in gene therapy, in generation antibodies that bind immunospecifically to NOVX substances for therapeutic or diagnostic methods. in

SO

Sequence 3201

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534

A; 1174 C; 986 G; 507 T; 0 other;

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Matches 16; Conserv
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                                                                                                 or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                     proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome molynucleotides may be used for detection of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                          Sequence
                                                                                                                                                                                                                                                                           AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                               Prostate cancer associated gene sequences, cancer antigens, useful for treatment, pre disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-)
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DB; AAB57000.
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ROSEN C A.
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                                                          3947
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM
30.8%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                          BP;
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                                                        983 G;
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26;
                             DB 21;
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RESULT 19
AAH34839/c
                                                                                                                                                                        the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps. CC by inserting the nucleic acids into a host cell and culturing the cell to express the protectine. N and P can be used in the prevention, diagnosis CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 CC present invention.
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                                                       Query Match
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Matches 16
                                                                                                                Sequence 3953
                                                                                                                                         \dot{N}.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3431-3432; 9803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999;
03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAG75434.
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                                                                    Similarity
                            CTCATCGCTCTCGTCG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
                                                        Conservative
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                                                                                                                ВP;
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99US-0163280.
                                                                                                              1055 A; 972 C; 986 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen
                                                                   30.8%;
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding cDNA SEQ ID NO:1921
                                                       0,
                                                                                  Score 16;
                                                                      Pred.
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                                                        Mismatches
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                                                                      No.
                                                                                  DB 22;
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                                                                                                                930 T; 10 other;
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RESULT

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AAS84163/c
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Best Local S
Matches 16
                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic a
genes from Drosophila
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      Homo sapiens
                                                                                                   DNA encoding novel human diagnostic protein #19967.
                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                      AAS84163 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 40961; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                   AAS84163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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11-JUL-2000; 2000US-0614150
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(ABB57737-ABB72072)
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Best Local S
Matches 16
  WO200171042-A2
                                      Drosophila melanogaster
                                                                           pharmaceutical;
                                                                                           Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                      Drosophila
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                                                                                                                                  melanogaster expressed polynucleotide SEQ ID NO 37040
                                                                                                                                                                           (first entry)
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gene;

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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WII at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase end in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7434 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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23-AUG-2000; 2000US-0649167
ABL14186 standard; cDNA; 15435 BP
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RESULT 23
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Matches 16; Conserv
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                                                                                                                                            Human; tweety homologue 2; TTYH2; therapy; cancer; tumour; cytostatic; diagnostic marker; gene; ds.
                                                                                                                                                                     Human tweety homologue 2 (TTYH2) gene.
                                                                                                                                                                                      14-MAY-2003
                                                                                                                                                                                                                       AAD52898 standard; DNA; 47999 BP
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL181676-ABL30511), expressed DNA sequences (ABL18167737-ABB72072).
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 37040; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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          /*tag= c
10377..10549
/*tag= d
/number= 2
10550..16622
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2075..10376
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1936..2074
                                                                                                    Location/Qualifiers
1946..45753
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P-PSDB; AAE34613.
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39563..40050
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39377.
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36685..38529
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36360..36591
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/number= 6
28976..35372
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16735..23223
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                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL3051), expressed DNA sequences (ABLIG176-ABL3051), expressed DNA sequences (ABLIG176-ABL3051), expressed DNA sequences (ABLIG175) and the encoded proteins
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                                                                                                                                                                        a fusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or retaring diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented products, ice-creams, fermented cereal based products, milk based based powers. Infant formula not food or a nharmacentical commonition
based powders, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, try tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bilidobacterium gene. ABQ81844 to ABQ81850 represent Bilidobacterium related nucleotide sequences given in the Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence given in least 90% identity or which hybridises with the sequences given in ABQ81843. Also described is a polynucleotide (II) encoding ABQ81842 and ABQ81843. Also described is a polynucleotide (II)
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identification; lactic acid bacterium; diarrhoea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 1100; 80pp;
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CC The present sequence describes a purified corn tassel-derived CC polynucleotide sequence (cdps) comprising a nucleic acid sequence CC selected from those given in ABL70627 to ABL76833. The cdps sequences CC selected from those given in ABL70627 to ABL76833. The cdps sequences (I) CC can be used for determining altered gene expression, to recover CC regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated CC with growth and development, disease resistance, environmental CC dispatched corn tassel-specific profile of gene transcription, a cc used to produce a tassel-specific profile of gene transcription, a cc used to produce a tassel-specific profile of gene transcription, a cc used to produce a tassel-specific profile of gene transcription, a cc used to produce a tassel-specific profile of gene transcription cc vectors, to express a polypeptide, to identify, isolate or extend contracted corn tassel nucleic acid sequences from DNA cc libraries, in nucleic acid hybridisation or amplification technologies,
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                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 4207;
                                                                                                                                                                                                                                                                                                                breeding programs
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adaptability; quality; yield; molecular marker;
it; plant breeding; corn tassel; gene; ss.
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RESULT 27
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Best Local
The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the abx17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1996;
03-DEC-1997;
09-SEP-1998;
                                                                                                                                                                                                                                                                                   New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets screening GM4,6D antagonists for treating e.g. arthritis, or tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular fucosylation; glycoconjugate fucosylation; transplant rejurchitis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                            Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
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97US-0984246.
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RESULT 28
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                                                                                                                                                                                                                                                                                                                                  ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in getherapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immune response, they can also be useful and preventional to the present invention and the prevention of the prevention o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 264 BP;
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                                                                                                                                          Sequence 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunogenic polynucleotides or polypeptides useful for diagnosing preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001US-280255P.
28-AUG-2001; 2001US-315563P.
09-JAN-2002; 2002US-347313P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S2 subtraction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 67; 207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in virology, immunology, m
recombinant DNA techniques
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                                                                                                                                                                                                                                                specification,
                                                                                                                                                                                                                                                                                                            techniques.
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                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed ification, but was obtained in electronic format directly from WIPO
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Pred. No.
                                                                                                                                      96 G;
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                                                                                                     4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, fucosylation, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences cenzyme, as well as in gene replacement therapy. Sequences human GM4,6D peptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular fucosylation; glycoconjugate fucosylation; transplant rej
arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
complex carbohydrate; gene replacement therapy; immunosuppressive;
antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                              Sequence 336 BP; 115 A; 49 C;
                                                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising a human 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1996;
03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 1259; 6pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1998;
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                                                                                           seqdata.uspto.gov/sequence.html
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                  Similarity
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97US-0984246.
98US-0149674.
99US-0333177.
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              Score 15;
Pred. No.
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94;
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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2000US-022950
2000US-022951
2000US-023043
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2000US-0246611
2000US-024621
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RESULT 31
ABK43452
ID ABK43
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Matches
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08-DEC-2000
09-DEC-2000
                                                                                                                                                                                                                                                                                                 (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, trachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, allzheimer's and Parkinson's diseases and cancers -
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                                                                                                                                                                                                                                     Local
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DB; AAU19744.
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15; Conserv
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2000US-0190076. 2000US-0198123. 2000US-0209467. 2000US-0209467. 2000US-0214886. 2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-02174887.

31.JAN-2000
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2000US-0229447 2000US-0225266 2000US-0225213 2000US-0225214 2000US-0225214 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225275 2000US-0225275 2000US-0225275 2000US-0225275 2000US-022575 2000US-022574 2000US-02274 2000US-02274

ABK43452 standard; cDNA; 357

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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
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17-JAN-2001; 02-AUG-2001.

2000US-0184664 2000US-0186350 2000US-0179065 2000US-0180628 2001WO-US01332

2000US-0189874

2000US-0231413

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13-OCT-2000
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2000US-0232397.
2000US-0232398.
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2000US-0232400.
2000US-0232401.
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                       New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and food additives or preservatives -
                                                                                                                                                                          Claim 1; SEQ ID No 42;
                                                                                                                                                                                                                     WPI; 2001-581633/65.
P-PSDB; AAU87122.
                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                           Barash SC,
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2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0249299.
2000US-0249300.
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2000US-0254097
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2000US-0256719
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2000US-0251030
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                                                                                                                                                                          837pp; English.
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used

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cc disorders e.g. neoplasms of the breast or live, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, cc angiogenesis, nervous system disorders e.g. Alzheimer's disease and cc amylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (Albs) and fungi, ocular disorders e.g. Acquired immunodeficiency virus (Albs) and fungi, ocular disorders c.g. dysphagia, cc adenocarcinomas and irritable bowel syndrome, reproductive system cc disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and productive disorders e.g. disorders e.g. disorders e.g. disorders e.g. control truitary dwarfism, cancers and disorders at the cellular level e.g. cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. crespiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cacute kidney failure and blood related disorders e.g. myocardial cc infarction. The polypeptides can also be used to aid wound healing and cepithelial cell proliferation, to prevent skin aging due to sunburn, to capital cell proliferation, to prevent skin aging due to sunburn, to contain organs before transplantation, for supporting cell culture of contain organs before transplantation, for supporting cell culture of contain organs before transplantation, for supporting cell culture of contains the content, lipid, protein, concrease or decrease storage capabilities, fat content, lipid, protein, The invention describes an isolated nucleic acid molecule (1) encoding a novel central nervous system protein. (1) and polypeptides (III) encoded by (1), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders.

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RESULT 32
ABQ66639
ID ABQ66
XX
AC ABQ66
XX
DT 23-AU
XX
DE Human
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                                                                                                                               S
                                                                                                                                                   Query Match
Best Local S
Matches 15
       Human polynucleotide SEQ ID NO 129
                           23-AUG-2002
                                                               ABQ66639
                                                                                                               102
                                                                                                                                                   1 Similarity
                                                                                                                         ATGCAGTTCTCTCAC 15
                                                               standard; cDNA; 357
                                                                                                             ATGCAGTTCTCTCAC 116
                                                                                                                                                  ilarity 100.0%;
Conservative 0;
                         (first entry)
                                                                                                                                                28.8%; Score 15; DB
100.0%; Pred. No. 94,
Live 0; Mismatches
                                                               ВP
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26-JUL-2000;
26-JUL-2000;
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14-AUG-2000;
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10-SEP-2000;
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07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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04-FEB-2000;
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gene; ss.
        Rosen
                                          (ROSE/)
(RUBE/)
(BARA/)
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        CA,
                                        ROSEN C A
RUBEN S M
BARASH S
        Ruben SM,
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2000US - 217495P
2000US - 22964P
2000US - 2294519P
2000US - 224519P
2000US - 22576P
2000US - 225787P
2000US - 225787P
2000US - 229287P
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New isolated diagnostics,
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The invention relates to novel genes (AB066521-AB066785) and proteins (AB047946-ABP48110) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discorders e.g. Addison's disease, allergies, autoimmune that allergies, autoimmune constitues, (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; and (f) infecti
and parasitic infections
Note: The sequence data i
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                                                                    WPI; 2001-639362/73
P-PSDB; ABG12221.
                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #12212.
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DB; ABP47964.
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upplement; medical imaging; diagnostic;
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polynucleotide and encoded polypeptides, forensics, gene mapping, identification of
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 T; 6 other;
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94;
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                    useful
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RESULT 34
AAZ19396/c
ID AAZ19396;
XX AAZ19396;
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XX O5-NOV-1999 (first of the control of the control
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Best Local
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispute the sequences have applications of the sequences have applications of the sequences.
New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                       WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis antigen 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 416 BP; 74 A; 118 C; 128 G; 96 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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98US-0025197.
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                                                                                                                                                                               Dillon DC,
SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSER-5 cDNA sequence
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                                                                                                                                                                                  Hendrickson RC, H
YAW, Twardzik DR,
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Pred. No.
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R, Vedvick TS
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RESULT 35
AAZ19184/c
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Best Local S
Matches 15
                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in success for diagnosis of tuberculosis and as reagents in success for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to
 Sequence
                                                                                                                                          Claim 11a; Page 274; 323pp; English.
                                                                                                                                                                       New polypeptide comprising antigenic portions of M.
                                                                                                                                                                                                                                                Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                         05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; detection;
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98US-0024753
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SG, Skeiky
95 A; 128
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                           re useful as vaccines for immunizing against ection. The new detection methods are needed strategies do not provide 100% immunity.
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100.0%;
 C; 129
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YAW, Twardzik!
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71
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94;
T; 0 other;
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R, Vedvick TS;
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                                                                                                                                                                        tuberculosis
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Query Match

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Length 423;

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RESULT 30
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Matches 15; Conser
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                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                            The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain, which is different from the first strain using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological samples. The polynucleotides identified are useful as probes or primers for detecting a given mycobacterium of interest. By aligning the polynucleotides contained in the recombinant BAC vectors it is possible to physically map a polynucleotide of mycobacterial origin in a biological sample. The methods and vectors from the present invention are useful in providing information for combating tuberculosis. It is
                                                                                                                                                                                                                                 possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABQ62492 to ABQ63228 and ABB81227 to ABB81230 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 44-45; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of detection of
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                                                                                                                                                                                                                   exemplification
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                                                                                     7
                                                                                                                                     Similarity
                                                                                                                                                                                     448
                                                                         TTCTCTCACGCTCTC 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTCGCTGCCGGCCT
                                                      TTCTCTCACGCTCTC 366
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                                                                                                                       Conservative
                                                                                                                                                                                     BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides from mycobacterial genomes, useful for \ensuremath{\mathsf{Mycobacteria}} and for combating tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis; Mycobacterium bovis; mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector; bacterial artificial chromosome; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9808-0060756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-IB00740
                                                                                                                                                                                                                  of the present invention.
                                                                                                                                                                                     67
                                                                                                                                                                                   A; 141 C; 133 G; 102 T; 5
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Pred. No.
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                                                                                                                                   DB 21;
94;
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                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity. Issue growth factor activity, immunomodulatory activity and activity, infinity activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundisorders -
     Human
                                   06-OCT-2000
                                                                                                                                                                                                                                                                                                              Sequence 459
                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 10333; 1399pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000;
18-MAY-2000;
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                                                                    AAC02001;
                                                                                                   AAC02001 standard; cDNA; 471
                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAO10342
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                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
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   secreted
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                                                                                                                                                                                 CTCTCATCGCTCTCG
                                                                                                                                                                                                              CTCTCATCGCTCTCG 31
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                                                                                                                                                                                                                                               Conservative
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2000US-0577409
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                                  (first entry)
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protein 5'
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
          30-JAN-2001; 2001WO-US00669.
                                     09-AUG-2001
                                                                                                                                                 Human foetal liver single exon nucleic acid probe #6943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                 WO200157277-A2
                                                                                        Homo sapiens
                                                                                                                  Human; foetal liver; gene expression; single exon nucleic
                                                                                                                                                                            01-FEB-2002
                                                                                                                                                                                                        ABA58638
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 471
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                                                                                                                                                                            (first entry)
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26-MAY-2000; 2000US-0608408.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
21-SEP-2000; 2000US-0234687.
21-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
Penn SG,
                                                                                                                                                                                   30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 481 BP; 73 A; 136 C; 180 G; 92 T; 0 other;
                                                                                                                                                           21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #6099 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52.
                                                    (MOLE-)
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XX
Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular disease,
CC Note: The sequence data for this patent did not form part of the printed
CC engenital heart disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
XX
Sequence 481 BP; 73 A; 136 C; 180 G; 92 T; 0 other;
Query Match
Best Local Similarity 100.0%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Query Match
Db 152 CGCTCTCATCGCTCT 29
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Sequence 242, Appli sequence 1, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 36, Appli sequence 1, Appli sequence 110, Appli sequence 1103, Appli sequence 1103, Appli sequence 5968, A sequence 5968, A sequence 5978, Appli sequence 5978, Appli sequence 5978, Appli sequence 5979, Appli sequence 5971, Appli sequence 5971, Appli sequence 6642, Appli sequence 6642, Appli sequence 6776, Appli sequence 5977, Appli sequence 5977, Appli sequence 5978, Appli sequence 5978, Appli sequence 6776, Appli sequence 7791, Appli sequence 77, Appli sequence 12, Appli sequence 1
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13272
LENGTH: 732
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13272
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US-09-252-991A-13107/c
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US-09-252-991A-13272/c
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Sequence 13107, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,791A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local
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US-09-252-991A-978
US-09-252-991A-978
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US-09-252-991A-3551
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US-09-252-991A-3551
US-09-252-991A-7927
US-09-252-991A-7927
US-09-252-991A-7927
US-09-252-991A-9057
US-09-252-991A-9057
US-09-252-991A-9059
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US-09-252-991A-9059
US-09-252-991A-9051
US-09-252-991A-9061
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7927, Ap
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6747, Ap
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GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO F

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NO 3602

IENOTH: 879

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3602
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3647
LENGTH: 810
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3647
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; Sequence 3647, Application US/09252991A
; Patent No. 6551795
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13107
LENGTH: 1056
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-3859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3859
LENCTH: 1632
Sequence 2686, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2993
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                Matches
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Patent No. 6551795
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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les 16; Conserv
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US-09-072-596-259/c
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US-09-252-991A-2875
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                             GENERAL INFORMATION:
APPLICANT: Reed, St
APPLICANT: Skeiky,
APPLICANT: Dillon,
APPLICANT: Campos-1
APPLICANT: Houghtor
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2875
LENGTH: 2814
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LENGTH: 2715
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                     APPLICANT:
APPLICANT:
APPLICANT:
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  OF INVENTION:
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                Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
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100.0%; Pred. No. 7.2;
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COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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NUMBER OF SEQUENCES:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASS/FICATION:
ATPORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                            SEQ ID NO 15918
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GENERAL INFORMATION:
                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                        LENGTH: 438
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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CITY: Seattle
STATE: Washingt
COUNTRY: USA
                                                                                      Local
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100.0%; Pred. No.
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                                                                      Mismatches
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US-09-670-314-60
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CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 60
LENGTH: 448
                                                                          Matches
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 60
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GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (various p
OTHER INFORMATION: a
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APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Billault, Alain

APPLICANT: Billault, Alain

TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/670,314
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-B
APPLICANT: Gordon, Step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 44
TYPE: DNA
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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FEATURE:
NAME/KBY: unsure
LOCATION: (various positions within the sequence)
COTHER INFORMATION: applicants are uncertain of bases designated
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No. 6492506
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                                                                        . Similarity 15; Conserv
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TTCTCTCACGCTCTC 366
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                                                                        Conservative
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                                                                                                                                                                 positions within the sequence) applicants are uncertain of bases
                                                                                      28.8%; Score 15;
100.0%; Pred. No.
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100.0%; Pred. No.
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27;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR IILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15774
LENGTH: 885
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-15804/c
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US-09-252-991A-15774/c
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Sequence 15804, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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GENERAL INFORMATION:
APPLICANT: Marc J.
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SEQ ID NO 15888
LENGTH: 762
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR RPILICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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26;
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Sequence 10603, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEU
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/4,788
PRIOR APPLICATION NUMBER: US/09/4,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 10603
LENGTH: 1146
TYGE TO NO 10603
LENGTH: 1146
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15804
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US-09-252-991A-10603/c
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US-09-252-991A-10788/c
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US-09-252-991A-10603
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10788
LENGTH: 1119
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15804
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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            ORGANISM: Pseudomonas aeruginosa
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25;
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; Sequence 168, Application US/09620312D
; Patent No. 6569662
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                          Sequence 10250, Application US/09252991A Patent No. 6551795
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 168
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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TITLE OF INVENTION: NO. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (96) .. (548)
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Liu, Chenghua
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Zhou, Ping
Ma, Yunqing
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Wang, Zhiwei
John Tillinghast
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Wehrman, Tom
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Yang, Yonghong
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100.0%; Pr
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-10368
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US-09-252-991A-10368
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Best Local Similarity
Matches 15; Conserva
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                               APPLICANT: MATC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPPUTICS
FILE REFERENCE: 107196.136
CURRENT PELLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10368
LENGTH: 1620
TYPE: DNA
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SEQ ID NO 11745
LENGTH: 1317
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SEQ ID NO 10250
LENGTH: 1260
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                   Patent No. 655179
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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ORGANISM: Pseudomonas aeruginosa
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100.0%; Pred. No.
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Query Match

Score 15;

DB 4;

Length 1620;

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RESULT 24
US-09-252-991A-108/c
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LENGTH: 2553
TYPE: DNA
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PATENT NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
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Best Local S
Matches 15
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Matches
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 1692
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                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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ORGANISM: Pseudomonas aeruginosa
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5183745-1
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NUMBER OF SEQUENCES: 13

CURRENT APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                       ;Patent No. 5183745
; APPLICANT: DANCHIN, ANTOINE;GLASER, PHILLIPPE;KRIN, EVELYN;
;BARZU, OCTAVIEN;LADANT, DANIEL;ULLMAN, AGNES
;TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
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                                                                                                                                      SEQ ID NO:1:
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LENGTH: 4198
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER DE SECTION SCIENCE

SECTIO
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APPLICANT: Levin, Joshua Z.
APPLICANT: Bauer, Michael W.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30909A
CURRENT APPLICATION NUMBER: US/09/586,719
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 34
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SEQ ID NO 108
          Query Match
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                         FILING DATE: 25-OCT-1989
                                                                                                       LENGTH: 4649
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100.0%; Pred. No. 24;
tive 0; Mismatches
   28.8%;
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   Score 15;
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23;
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Length 4649;
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RESULT 28
US-08-669-785-1/c
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                                                                                                                                                                                                                                                                                             US-08-669-785-3
               Sequence 1, Application US/08669785 Patent No. 6309648 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,785
FILING DATE: 27-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0072-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches 15; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow,
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Betsou, Fotini
APPLICANT: Sebo, Peter
APPLICANT: Guiso, Nicole
TITLE OF INVENTION: Protective Epitopes Of Adenyl
TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To
TITLE OF INVENTION: The Treatment Or To The Prevention Of Bordetella Infections.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
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CITY: Washington
                                                                                                                                                                                                                    Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5118 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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Betsou, Fotini
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                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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RESULT 29
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                                                                                                                                                            BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                SEQ ID NO:5:
                                   Matches
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Best Local
                                               Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,785
FILING DATE: 27-JUN-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                 APPLICANT: DANCHIN, ANTOINE;GLASER, PHILLIPPE;KRIN, EVELYN;
ZU, OCTAVIEN;LADANT, DANIEL;ULLMAN, AGNES
TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protective Epitopes Of Adenyl TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To TITLE OF INVENTION: The Treatment Or To The Prevention Of Bordetella
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LCCATION: 979..6096
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: (
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                                                                                                                  LENGTH: 6443
                                                                                                                                                  FILING DATE: 25-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 6441 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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34 GCTGCCGGCCTCGCC
                               l Similarity
15; Conserv
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Guiso, Nicole
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                                 Conservative
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                        28.8%; Sur
100.0%; Pr
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100.0%; Pred. No.
tive 0; Mismatc
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                                               Score 15;
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                                   Mismatches
                                             DB 6;
22;
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22;
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US-09-922-445-1
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US-09-453-702B-242/c
US-09-453-702B-242/c
Sequence 242, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
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                                                     GENERAL INFORMATION:
APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. '
APPLICANT: Reneland, Rikard I
APPLICANT: Adam, Gail I. R.
                                                                                                                                              Sequence 1, Application US/09922445 Patent No. 6528268
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                   TITLE OF INVENTION: REAC
     CURRENT
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INFORMATION FOR SEQ ID NO: 242:
                                                                                                                                                                                                                                                         26165 TCGCTCTCGTCGCTG 26151
                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blattner, Frederick
APPLICATION NUMBER: US/09/922,445
                                                                                                                                                                                                                                                                             23 TCGCTCTCGTCGCTG 37
                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: ~Unknown>
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     Berglund, Lars G. T.
Reneland, Rikard H.
Adam, Gail I. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 31880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 8.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Madison
                                                                                                                                                                                                                                                                                                                             28.8%; Score 15; DB 4; Length 31880; larity 100.0%; Pred. No. 19; Conservative 0; Mismatches 0; Indels
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Plunkett, ou,
Plunkett, ou,
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                                    REAGENTS AND METHODS FOR DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (608) 251-5000
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                                    OF HEART
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NAME/KEY: Intron
LOCATION: (32529)..(33414)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (32614)..(32614)
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can
OTHER INFORMATION: A or G
                                                                                                                                                                                                                             LOCATION: (32163)...(
OTHER INFORMATION: r
OTHER INFORMATION: A
NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-08-0
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (32163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (24941)..(24941)
OTHER INFORMATION: nucleot
OTHER INFORMATION: T or C
                                                                                                                                                                                                LOCATION: (32401).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
NAME/KEY: Intron
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: (31748)..(31841)
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (31028)
OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (30895)..(31027)
OTHER INFORMATION:
NAME/KEY: Intron
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LOCATION: (308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Intron
LOCATION: (30682)..(30894)
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OTHER INFORMATION:
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LOCATION: (27645)..(27645)
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NOCATION: (27179)..(30519)
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OTHER INFORMATION:
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LOCATION: (24801)..(24801)
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OTHER INFORMATION:
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OTHER INFORMATION
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                                                                                                                                                                                                                                               nucleotide 32163 is a single nucleotide polymorphism which can A or \ensuremath{\mathsf{C}}
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T or C
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C or G
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RESULT 32
US-08-804-227C-7
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sucton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
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DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..(38653)
                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (34315)..(34588)
OTHER INFORMATION:
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LOCATION: (38342)..(38653)
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LOCATION: (36524)..(38341)
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OTHER INFORMATION:
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LOCATION: (34589)..(36404)
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OTHER INFORMATION:
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                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-6
                   SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pai
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44377 base pairs ucleic acid
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100.0%; Pred. No. 19
tive 0; Mismatches
                                                                                                                  X-8231
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US-08-804-198-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                        APPLICATION NUMBER: US/08/804.
FILING DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REGISTRATION NUMBER: 36,470
                                                                                                                  TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
FEATURE:
                                          LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macinto
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ADDRESSEE: PAUL R. CANTRELL 1:
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
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NAME/KEY:
                               FEATURE:
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APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
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 NAME/KEY:
LOCATION:
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350..14002
CDS
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                                            DNA (genomic)
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19;
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-804-198-1
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US-09-568-102-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1
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                                                                                                                                                                                                                                         Sequence 1, Application US/09568102 Patent No. 6346404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.8%; Score 15; DB 3; Best Local Similarity 100.0%; Pred. No. 18; Matches 15; Conservative 0; Mismatches
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       APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Moinar, Istvan
APPLICANT: Moinar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Gyr, Devon
APPLICANT: Gyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR PILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Moinar, Istvan
APPLICANT: Moinar, Istvan
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-10582A
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
NUMBER OF SEQ ID NOS: 30
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; SEO ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1
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US-09-567-969-1/c
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                                                     APPLICANT: CYr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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Best Local Similarity
Matches 15; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
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PRIOR FILING DATE: 1999-06-17
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TYPE: DNA
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Zirkle, Ross
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Goetlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
SOFTWARE: PATENTING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
TYPE: DNA
CORANISM: Sorangium cellulosum
US-09-568-472-1
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US-09-568-486-1/c
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SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
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Patent No. 6358719
  Query Match 28.8%; Score 15; DB 4; Length 68750; Best Local Similarity 100.0%; Pred. No. 18; Matches 15; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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Search completed: November 13, 2003, 10:59:54 Job time: 79 secs
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                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
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Best Local :
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                                                                                                                                                                                                                                                                                                           APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                                                                                                                  Local Similarity
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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APPLICANT: Williams, Spencer J.

APPLICANT: Williams, Spencer J.

APPLICANT: Williams, Spencer J.

APPLICANT: Mougous, Joseph

TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins

TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins

TITLE OF INVENTION: Wycobacterial Sulfation Pathway Proteins

TITLE OF INVENTION: Wycobacterial Sulfation Pathway Proteins

TITLE OF INVENTION: Mycobacterium Avium

PRIOR APPLICATION NUMBER: US/10/286,606

CURRENT FILING DATE: 2002-0-31

PRIOR APPLICATION NUMBER: 60/285,394

PRIOR APPLICATION NUMBER: 60/345,953

PRIOR APPLICATION NUMBER: 60/345,953

PRIOR APPLICATION NUMBER: 10/126,279

PRIOR APPLICATION NUMBER: 10/126,279

PRIOR FILING DATE: 2002-04-19

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

SEQ ID NO 11

LENGTH: 1392

TYPE: DNA

ORGANISM: Mycobacterium avium

PRATURE:
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; Publication No. US20030180321A1
    Query Match 32.7%; Score 17; DB 12; Length 1392; Best Local Similarity 100.0%; Pred. No. 4.9; Matches 17; Conservative 0; Mismatches 0; Indels
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US-10-127-833A-417
US-10-127-834A-417
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US-10-127-836A-417
US-10-128-687A-417
US-10-128-687A-417
US-10-128-689A-417
US-10-128-699A-417
US-10-131-825A-417
US-10-131-825A-417
US-10-131-815A-417
US-10-131-815A-417
US-10-131-815A-417
US-10-131-827A-417
US-10-131-935A-417
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US-10-131-935A-417
US-10-131-935A-417
US-10-131-935A-417
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US-10-123-912-417
US-10-1192-007-417
US-10-1192-007-417
US-10-1192-007-417
US-10-117-847A-417
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                                                                                                                         Sequence 25977, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

ITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION SUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FSatSEQ for Windows Version 3.0

SEQ ID NO 25977

LENGTH: 574

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1):..(574)

OTHER INFORMATION: n = A,T,C or G
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GENERAL INFORMATION:
APPLICANT: Milliams, Spencer J.
APPLICANT: Milliams, Spencer J.
APPLICANT: Milliams, Spencer J.
APPLICANT: Muggus, Joseph
ITITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins
ITITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins
ITITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins
ITITLE REFERENCE: BERK-012
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/285, 394
PRIOR APPLICATION NUMBER: 60/285, 394
PRIOR APPLICATION NUMBER: 60/285, 394
PRIOR APPLICATION NUMBER: 60/345,953
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEO ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-918-995-25977
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LENGTH: 1392
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TYPE: DNA
ORGANISM: Mycobacterium avium
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1392)
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                                                                   Query Match
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                                               Conservative
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100.0%; Pr
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k; Pred. No. 20;
0; Mismatches
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                                                                DB 11;
20;
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RESULT 6
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; NAME/KEY: CDS
; LOCATION: (1)...(1653)
US-09-897-214-7
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US-09-897-214-7
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Best Local S
Matches 16
Sequence 189, Application US/10093463
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/22350
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/148,759
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application of Patent No. US20020012966A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                 LENGTH: 1872
TYPE: DNA
ORGANISM: Homo sapiens
-09-768-826-21
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/768,826
CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shi et al.
TITLE OF INVENTION: 18
FILE REFERENCE: PF512P1
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CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thayer, Edward C.
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell Scott R.
TITLE OF INVENTION: Leucine-Rich Repeat Proteins,
TITLE OF INVENTION: Zlrr8, and Zlrr9
FILE REFERENCE: 01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                            1496 CGCTGCCGGCCTCGCC 1511
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                                                                                                                                                l Similarity 100.
16; Conservative
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                                                                                                                                                              30.8%; Score 16; 100.0%; Pred. No.
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                                                                                                                                                Mismatches
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17;
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PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/287,424
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/299,027
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/309,198
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/281,194
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/283,675
PRIOR FILING DATE: 2001-04-14
PRIOR APPLICATION NUMBER: 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,101
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR APPLICATION NUMBER: 60/304,354
PRIOR APPLICATION NUMBER: 60/304,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20030208039A1 GENERAL INFORMATION:
PRIOR
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Taupier, Raymond J. Jr.
TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypepi
TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
FILE REFERENCE: 21402-290A (Cura 590AT)
CURRENT APPLICATION NUMBER: US/10/093,463
CURRENT FILING DATE: 2002-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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        OR PELLING DATE: 2001-03-08
OR FILING DATE: 2001-03-08
OR APPLICATION NUMBER: 60/274,849
OR APPLICATION NUMBER: 60/274,849
OR APPLICATION NUMBER: 60/330,380
OR FILING DATE: 2001-10-18
OR APPLICATION NUMBER: 60/275,235
OR FILING DATE: 2001-03-12
OR APPLICATION NUMBER: 60/288,342
OR APPLICATION NUMBER: 60/288,342
OR APPLICATION NUMBER: 60/275,578
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-07-10
APPLICATION NUMBER: 60/279,995
FILING DATE: 2001-03-30
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Kekuda, Ramesh
Gusev, Vladimir
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Tchernev, Velizar
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Vernet, Corine
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Spytek, Kimberly
Gorman, Linda
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Rastelli, Luca
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Miller, Charles
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Anderson, David
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APPLICANT: Patturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Taupier, Raymond J. Jr.
TITLE OF INVENTION: No. US20030208039A1el Antibodies that Binder Street S
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; NAME/KEY: CDS
; LOCATION: (471)..(2169)
US-10-093-463-189
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 189
LENGTH: 2451
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Best Local Similarity 100.0%;
Matches 16; Conservative
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Publication No
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ORGANISM: Homo sapiens
APPLICATION NUMBER: 60/304,354 FILING DATE: 2001-07-10
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Gorman, Linda
Spaderna, Steven
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Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
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Anderson, David
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Casman, Stacie
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Kekuda, Ramesh
Gusev, Vladimir
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Rastelli, Luca
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f Use.
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PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/294,899
PRIOR APPLICATION NUMBER: 60/287,424
PRIOR APPLICATION NUMBER: 60/287,424
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/299,027
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/291,194
PRIOR PRILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR APPLICATION NUMBER: 60/30,380
PRIOR FILING DATE: 2001-03-18
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR PRILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/275,535
PRIOR FILING DATE: 2001-03-13
PRIOR PRILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-13
PRIOR PRILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 370
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 191
LENGTH: 2563
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US-10-246-330-1
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                                                                                             US-10-246-330-1
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/323,241
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2610
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10246330
Publication No. US20030166030A1
GENERAL INFORMATION:
APPLICANT: O'Toole, George A.
APPLICANT: Mah, Thien-Fah
TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
TITLE OF INVENTION: BIOFILM-SPECIFIC ANTIBIOTIC RESISTANCE
FILE REFERENCE: 14537-002001
CURRENT APPLICATION UMBER: US/10/246,330
CURRENT FILLING DATE: 2002-09-18
CURRENT FILLING DATE: 2002-09-18
                                                                                                 LENGTH: 2610
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2607)
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Best Local Similarity
    Matches
                       Query Match
Best Local (
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NAME/KEY: CDS
LOCATION: (130)..(2464)
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16;
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                          Similarity
  Conservative
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                       30.8%; Score 16; 100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/274,101
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR APPLICATION NUMBER: 60/325,681
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/279,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Taupier, Raymond J. Jr.
TITLE OF INVENTION: No. US20030208039Alel Antibodies that Bind to Antigenic Polypepti
TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
FILE REFERENCE: 21402-290A (Cura 590AT)
CURRENT APPLICATION NUMBER: US/10/993,463
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/283,675
PRIOR FILING DATE: 2001-04-14
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                                                                                                    APPLICATION NUMBER: 60/309,198
FILING DATE: 2001-07-31
APPLICATION NUMBER: 60/281,194
FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/274,194
                                                                                FILING DATE: 2001-03-08
                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/299,027
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/287,424 FILING DATE: 2001-04-30
                         APPLICATION NUMBER: 60/274,849 FILING DATE: 2001-03-09
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Kekuda, Ramesh
Gusev, Vladimir
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Miller, Charles
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Gorman, Linda
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Casman, Stacie
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Anderson, David
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Vernet, Corine
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Tchernev, Velizar
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60/330,380
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RESULT 11
US-10-106-698-1931/c
US-10-106-698-1931/c
; Sequence 1931, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptic
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILLING DATE: 1999-03-12
PRIOR FILLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
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PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/275,578
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3947
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (471)..(2412)
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (3738)
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APPLICATION NUMBER: 60/275,235
FILING DATE: 2001-03-12
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16; Conservative
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Pred. No.
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Or
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15;
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RESULT 13
US-09-878-574-15763/c
· Sequence 15763, Application US/09878574
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SOFTWARE: PERL E
SEQ ID NO 4207
LENGTH: 214
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Best Local :
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SEQ ID NO 1931
LENGTH: 3953
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Best Local
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700353417H1
NAME/KEY: unsure
LOCATION: 10, 37, 204
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ORGANISM: Zea mays
FEATURE:
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LOCATION: (618)..(618)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (626)..(626)
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30.8%; Score 16;
Local Similarity 100.0%; Pred. No.
hes 16; Conservative 0; Mismatc
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15; Conserv
                                                                                                                     ATGCAGTTCTCTCAC 196
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                                                                                                                                                                                      28.8%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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April 21, 1998
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RESULT 15
US-09-878-574-1259/c
; Sequence 1259, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(294)
US-10-156-761-711
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; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORWATION: Clone ID: 701070483H1
US-09-878-574-15763
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US-10-156-761-711/c
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 711
LENGTH: 294
TYPE: DNA
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PRIOR FILING DATE: 199-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15763
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Best Local :
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                                                                                                                                    143 TCGTCGCTGCCGGCC 129
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15; Conservative
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HORIKAWA, HIROSHI
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b. US20030119018A1
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                           DB 14; Length 294; 76;
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78;
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RESULT 17
US-10-125-540-129
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; ORGANISM: Homo sapiens
US-09-764-870-129
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US-09-764-870-129
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; ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-A1
US-09-878-574-1259
US-10-125-540-129
                                                                                                                                           Sequence 129, Application US/1012540
Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: P7214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-117
CURRENT FILING DATE: 2001-117
         Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 129
LENGTH: 357
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT PLING DATE: 105/01-12-21
PRIOR APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1259
LENGTH: 336
TYPE: NNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 129
LENGTH: 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 28.8%; Score 15; DB
Local Similarity 100.0%; Pred. No. 74
hes 15; Conservative 0; Mismatches
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nes 15; Conserv
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100.0%;
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Pred. No.
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74;
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US-10-084-843-264
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                                                                      Matches
                                                                                                      Query Match
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Best Local
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INFORMATION FOR SEQ ID NO: 264
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION - cunknown>
PRIOR APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
                                                                    Local Similarity
les 15; Conserv
                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION. CAMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED an
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 26
                                30 CGTCGCTGCCGGCCT 44
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CGTCGCTGCCGGCCT 12
                                                                                                                                                                                                  LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington
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STREET: 6300 Columbia Center,
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                                                             28.8%; Score 15; DB 12; Length 423; ilarity 100.0%; Pred. No. 73; Conservative 0; Mismatches 0; Indels
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Dillon, Davin C.
Campos-Neto, Antonio
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RESULT 19

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RESULT 20
US-10-259-678-60
; Sequence 60, Application US/10259678
; Dublication No. US20030198974A1
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                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
                                                                                       APPLICANT: Cole, Stewart APPLICANT: Buchrieser-B
                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
APPLICATION NUMBER: US/10/193,002
CINCERETORYON. (INCOMPA
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Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
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MEDIUM TYPE: Floppy disk
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                                                                                                                           INFORMATION
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                                                    Gordon, St
Billault,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ULE TYPE: cDNA
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                                                                                     Buchrieser-Brosch, Roland
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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                                                                      Stephen
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CURRENT APPLICATION NUMBER: US/10/259,678
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure LOCATION: (various OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 448
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                         OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00666
                                      DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00662

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00661

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00670

DR APPLICATION NUMBER: PCT/US01/00670

DR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TICTCTCACGCTCTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
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                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115584
RESULT 23
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PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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Best Local S
Matches 15
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Publication NO. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

FILE REFERENCE: 108827.129
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6099
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 603
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                                                                     48
                                                                                                                    25 GCTCTCGTCGCTGCC 39
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                                                                     GCTCTCGTCGCTGCC 62
                                                                                                                                                                     Conservative
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                                                                                                                                                                                         28.8%; Score 15; DB 12; Length 603; 100.0%; Pred. No. 69;
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                                                                                                                                                                  Mismatches
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APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2011-204089
PRIOR TILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 974
LENGTH: 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 603
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115584
                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1113)
US-10-156-761-974
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PRIOR PRIOR DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
PRIOR FILING DATE: 1999-08-09
NUMBER: F85-550 for Mindres US 60/146,002
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         Matches
                                                   Query Match
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Best Local
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                           TYPE: DNA ORGANISM: Streptomyces avermitilis
                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GCTCTCGTCGCTGCC
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       l Similarity
15; Conserv
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    Conservative
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28.8%; Score 15;
100.0%; Pred. No.
tive 0; Mismatch
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Pred. No.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                          DB 14; Length 1113;
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  Gaps
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CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR PILING DATE: 2002-03-27
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta SEQ ID NO 279
; LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-279
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US-10-037-270-168/c
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US-10-259-165-279
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Wang, Xun
APPLICANT: Chang, Hux
APPLICANT: Briggs, St
APPLICANT: Glazebrook
APPLICANT: Goff, Step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 168, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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APPLICANT:
APPLICANT:
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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APPLICANT: Ricke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
                                                                              APPLICANT:
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       INVENTION: No.
: Xue, Aidong J.
: Yang, Yonghong
: Wang, Jian-Rui
: Zhou, Ping
: Ma, Yunqing
: Ma, Yunqing
: Wang, Dunrui
: Wang, Zhiwei
: Tillinghast, John
: Drmanac, Radoje T.
INVENTION: No. US20030104529Alel Nucleic Ac
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Moughamer, luca
Mougham
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Briggs, Steven P.
Cooper, Bret
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Goff, Stephen A.
Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10037270
5. US20030104529A1
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o. US20030135888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.8%; Score 15; DB llarity 100.0%; Pred. No. 63 Conservative 0; Mismatches
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63;
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       Acids
   and
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; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo Bapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)..(548)
US-10-037-270-168
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CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 168
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                                                                                                                                                   ; TYPE: DNA; ORGANIAM: Streptomyces avermitilis; FEATURE: NAME/KEY: CDS; LOCATION: (1)..(1389)
US-10-156-761-780
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAHBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                          SEQ ID NO 780
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                                                                                                              Query Match
                                                                           Matches
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Best Local S
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                     LENGTH: 1389
                                                                                              Local
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                30 CGTCGCTGCCGGCCT 44
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                                                                       Similarity 100.0%; 1
15; Conservative 0;
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Similarity 100.0%; Pred. No.
15; Conservative 0; Mismatch
CGTCGCTGCCGGCCT
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                                                                                         28.8%; Score 15; DB 14; Length 1389; 100.0%; Pred. No. 61;
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                                                                       Mismatches
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US-10-177-293-416/c US-10-177-293-416/c ; Sequence 416, Application US/10177293 ; Publication No. US20030124128A1 ; GENERAL INFORMATION:

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          APPLICANT: ISHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHTRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-10-177-293-416
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Best Local Similarity
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LENGTH: 1404
SEQ ID NO 4461
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APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
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PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
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PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
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PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
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Hortobagyi, Gabriel
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Meyers, Rachel E.
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Kamatkar, Shubhangi
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US-10-128-714-6070/c
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; LOCATION: (1)..(1479)
US-10-156-761-4461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-3
PRIOR FILING DATE: 2001-04-3
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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SEQ ID NO 7070
LENGTH: 1554
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APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lenieux, Sebastien M
APPLICANT: Lenieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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          APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION:
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15; Conservative
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15; Conserv
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/ 100.0%; Pr
    Methods of Use
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Pred. No.
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                                                                                                                                         ; ORGANISM: Penicillium chrysogenum US-09-801-368-235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Aspergillus fumigatus 
US-10-128-714-6070
                                                                                                    Query Match
                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 6070
LENGTH: 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                            APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR PPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR RILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/295,890 PRIOR FILING DATE: 2001-06-05 PRIOR ELING DATE: 2001-07-09 PRIOR ELING DATE: 2001-07-09 PRIOR APPLICATION NUMBER: US 60/316,362 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Busby, nounce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-801-368-235/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                            LENGTH: 1932
                                                                                     Local
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1024 TCTCATCGCTCTCGT 1010
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15; Conserv
                                                                    Similarity
15; Conserv
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Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
No. US20020128250Alman, 7
                                  TCTCATCGCTCTCGT 32
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Silva, Jeff
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Salama, Sofie
                                                                    Conservative
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                                                              100.0%; --
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                                                                                 Score 15;
; Pred. No.
                                                                    Mismatches
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-6-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2978
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                                                                                                                          ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2412)
US-10-156-761-158
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
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US-10-156-761-158
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SEQ ID NO 158
LENGTH: 2412
TYPE: DNA
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                                             Matches
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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Publication No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                        ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                              Local
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  28 CTCGTCGCTGCCGGC 42
                                           l Similarity
15; Conserv
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                                           Conservative
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                                  28.8%; 5C
100.0%; Pr
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                                                            Score 15;
Pred. No.
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                                           Mismatches
                                                            DB 14;
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1471 CTCGTCGCTGCCGGC 1485

US-09-815-242-4138

GENERAL INFORMATION:

Sequence 4138, Application US/09815242 Patent No. US20020061569A1

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RESULT 36
US-09-374-046A-125
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Best Local
                                                                                                                                                                                                                      APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
APPLICANT: Evans, Cheryl
                                                                                                           APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
                                                                                                                                                                                  APPLICANT: Merberg, David APPLICANT: Treacy, Maurice
CURRENT APPLICATION NUMBER: US/09/374,046A
                   APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GI 6075-83A
                                                                                                                                                                    APPLICANT: Agostino, Michael J.
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                           APPLICANT:
                                                                                             APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-10-23
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                                                                                                                                                                                                                            Collins-Racie, Lisa A. Evans, Cheryl
                                                                           Fechtel, Kim
                                                                                           Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                           Application US/09374046A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 125
; SEQ ID NO 125
; LENGTH: 2672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-374-046A-125
                                                                                                      RESULT 38
US-09-967-768A-182/c
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SEQ ID NO 518
LENGTH: 2790
TYPE: DNA
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Sequence 182, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
                                                                                                                                                                                                                                                                                                         Query Match
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Best Local :
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PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, Paul
TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
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                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                       28.8%;
Local Similarity 100.0%;
les 15; Conservation
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CURRENT APPLICATION NUMBER: US/60/236,109
CURRENT PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
SOFTWARE: PATENTIAL PA
RESULT 40
US-09-822-846-197
; Sequence 197, Application US/09822846
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
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US-10-128-714-70/c
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Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 197
LENGTH: 3323
TYPE: DNA
ORGANISM: Homo sapiens
Search completed: November 13, 2003, 11:54:39 Job time : 246 secs
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Matches
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APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
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Fechtel, Kim
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Steininger II, Robert J.
Bowman, Michael R.
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Treacy, Maurice
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AUU3164766 AUU3164766
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AV61301 T3 end of BM47083 AGENCOURT
AU271547 Tetraodon
B2759663 Tetraodon
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Result No.

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BIO3345 CM4-M BO754769 EBed0 BG054345 OV2-3 BG054345 OV2-3 BG054345 OV2-3 BG054345 OV2-3 BG054345 OV2-3 BG054345 OV2-3 BG054360 PLANJF BM826925 AV8186 AV422875 AV8186 AV422875 AV4228 BW4422875 AV4228 BW4422875 AV4227 BW40773 AV4077 AV4014697 AV4077 AV401496 AV4277 AV4014697 AV41469 BW4642727 mgmko AV427304 AV4273 BW4941650 AV4140 BW466196 AV4243 BW4941650 AV4140 BW466196 H114E BW79464 AV40707 BW79464 AV40707 BW79464 AV40707 BW79466 BW609 BW797946 AG-ND BW797946 AG-ND BW797946 BW1099 BW1097944 BBm00 BW7979796 AG-ND BW797996 BW1099 BW797990 BW797996 BW1099 BW797990 BW79990 BW79990 BW79990 BW79990 BW79990 BW79990 BW79990 BW79990 BW799
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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1 (bases 1 to 395)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis sph
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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1 (bases 1 to 401)

Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
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immitis cDNA clone CIABB70 5' sequence, mRNA sequence.
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Email: gardner@tigr.org.
Location/Qualifiers
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BF252856.1 GI:16932999
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                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 557)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA li
                                                                                                          9712 Medical Cent
Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                        Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
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BF252723.1 GI:16932866
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 531)

Gardner, M. J. and Kirkland, T.
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                                                                                                                                                                                                           Unpublished
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Location/Qualifiers
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Generation of ESTs from Coccidioides
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301 838 0208
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                                                                             gardner@tigr.org.
Location/Qualifiers
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Paracoccidioides brasiliensis
Paracoccidioides brasiliensis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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EST08290 Pb0001
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 737)
Gardner, M.J. and Kirkland, T.
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Location/Qualifiers
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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BF251103.1 GI:16931246
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Contact: Malcolm J. Gardner
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1 (bases 1 to 133)
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The Paracoccidioides brasiliensis EST genome project Eukaryotic Cell, (2002) In press (Contact: Gustavo Henrique Goldman Laboratory of Molecular Biology Universidade de Sao Paulo - USP - FCFRP Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Prail Contact - SP, Resil. Cellanne Preto - SP, Prail Contact - SP, Resil. Cellanne Preto - SP, Prail Contact 
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BP112708 ORCS bovine utero-placenta
ORCS13477 5', mRNA sequence.
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Mol. Reprod. Dev. 65 (1), 9-18 (2003)
                                                                                                                                                                                                  Email: gtsujimoto@nch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System (ORG)
) project of Ministry of Education, Culture, Sports, Science and
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
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88 c 59 g 91 t
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/clone="ORCS13477"
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Oryza sativa (japonica cultivar-group)
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Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AU163553 Rice panicle at flowering stage Oryza sativa cultivar-group) cDNA clone E1586, mRNA sequence.
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AU166766.1 GI:12405165
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National Institute of Agrobiological Resources
Program. Kannondai 2-1-2,
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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/clone_lib="ORCS bovine
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/note="Organ: panicle; Rice
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Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 468)
                                                                                                                                                                                                                                              Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone R2118_6Z, mRNA sequence.
AU031845
AU031845.1 GI:3767818
EST.
                                                                                                                                                                                                                                                                                   305-8602,
                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                       Minobe, Y. and Sasaki, T. Rice cDNA from root
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Contact: Takuji Sasaki
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                                                                                                                                                                                                             PROJECT ='RGP'
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                      /organism="Oryza sativa (japonica cultivar-group)"

mol type="mRNA"

/cultivar="Nipponbare"
/db xref="reaxon.39947"
/clone="R2118 62"
/clone="R2118 62"
/clone="b="Rice root"
/note="Prepared from seedling root. "
                                                                                                                                                                         Location/Qualifiers
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|mol type="mRNA"
|cultivar="Nipponbare"
|db xref="taxon:39947"
|clone="C50247"
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/clone_lib="Rice callus (2001)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Fax: 864 656 4293
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ510461.1 GI:4733065
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                                                                                                                                                            // Clone lib="CUGI Rice BAC Library"
// Clone library library library source of the world world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional Cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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/lab_host="E. coli
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/mol_type="genomic DNA"
/strain="Japonica"
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                                            767 bp mt IpCGJx14_9_G08_23 IpCGJx14 Ictalurus IpCGJx14_9_G08_5', mRNA sequence. CB939902 CB939902.1 GI:30225293 EST.
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Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta;
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OSJNEf13003.r OSJNEf Oryza sativa (japonica cultivar-group)

clone OSJNEf13003 3', mRNA sequence.
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BACKWARD: gga aac agc tat gac cat
Plate: 13 row: O column: 03
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Contact: Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jantasuriyarat, C., Lu,G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         /clone lib="OSJNEf"
/note="Vector: pBluescript II KS
XhoI; Uninfected Control"
246 c 198 g 177 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
|mol type="mRNA"
|cultivar="Nipponbare"
|db_xref="taxon:39947"
         punctatus
                      punctatus (channel catfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="OSJNEf13003"
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ORGANISM
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BE039817/c
LOCUS
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   FEATURES
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Best Local
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                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 978)

1 (bases 1 to 978)

1 (bases 1, Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferre, H., J., Borchert, C., Brazille, S., Mcoks, J., Eaton, M., Ferre, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance
                                                                                                   University of Arizona
Bio Sciences West room 513,
                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                    Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                        BE039817
OC08E11 OC Oryza sativa
BE039817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: gwaldbieser@ars.usda.gov
Single pass sequencing. Bases called with Phred v0.000925.c.
quality bases and vector trimmed with Lucy v1.16.
Plate: 9 row: G column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 Experiment Station Road, Stoneville, Tel: 662 686 3593 Fax: 662 686 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Waldbieser GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bengten, E., Khayat, M., Middleton, D., Waldbieser, G., Askovic, S., Jensen, K.T., Warr, G., Miller, N., Clem, L. W. and Wilson, M. Identification of expressed genes in mixed leukocyte culture and a macrophage cell line in channel catfish, Ictalurus punctatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
                                                                                                                                        Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catfish Genetics Research Unit USDA-Agricultural Research Service
Best blastx match: 'emb|CAA16536.1| (AL021633) predicted protein
[Arabidopsis thaliana] 51 le-05'. An open reading frame exists.
    Location/Qualifiers
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                                                                      520-621-7982
520-621-1697
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                                                     cbm@u.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IpCGJx14_9 G08"
/cell type="macrophage"
/cell line="42TA"
/dev stage="adult"
/lab_host:"UH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="IpCGJx14"
/note="Vector: pSport1; Site_1: Sal 1; Site_2: Not 1;
Primary library"
169 c 271 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="commercial"
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/mol_type="mRNA"
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Best Local 3
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Best Local Similarity
Matches 19; Conserv
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                                                                                                              Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1712)
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BG163853.1 GI:12670556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                              169
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                                                                                                                Conservative
                                                                                                                                                                                                                   /db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:4453297"
/tissue_type="hypernephroma, cell line"
/lab_host="bull0B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_l: NotI;
/note="organ: hidney; Vector: 
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/tissue_type="roots"
/dev_stage="1 week"
/clone_lib="0C"
/note="no_stress"
a 188 c 313 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
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/mol_type="mRNA"
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100.0%; Prr
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                                                                                                                                   Score 19; DB 10; Length 1712; Pred. No. 10;
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Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing, and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim_wustl,edu) and/or Stephen M. Beverley Ph.D.
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Contact: Akopyants, NS /
WashU Leishmania Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J.C., Roos, D.S. and Beverley, S.M.
A survey of the Leishmania major Friedlin strain V1 genome by Shotgun sequencing: a resource for DNA microarrays and expression
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Fax: 314 286 1810
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368 bp DNA linear GSS 25-MAY-20:
LMAJFV1_lm25f07.yl Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lm25f07 5', genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /clone="LMAJFV1 lm25f07"
/lab host="TOP10 (Invitrogen)"
/clone_lib="Leishmania major FV1 random genomic library"
/clone_tib="Leishmania major FV1 random genomic library"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site."

94 c 123 g 61 t
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/mol_type="genomic DNA"
/strain="Friedlin strain V1"
/db_xref="Laxon:5664"
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100.0%; Pr
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Pred. No. 24;
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                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 558)
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Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
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RH22614.5prime RH Drosophila melanogaster normalized Head p
Drosophila melanogaster cDNA clone RH22614 5, mRNA sequence
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18; Conserv
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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Drosophila melanogaster cDNA clone RH40331 5, mRNA sequence.
BI568671
BI568671.1 GI:15460093
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/clone lib="RH Drosophila melanogaster normalized Head
pFlc-1"
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148 c 176 g 120 t 2 others
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/db xref="taxon:7227"
/clone="RH40331"
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Query Match
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Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 bp mRNA linear EST 07-SEP-2 RH67006.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH67006 5 mpwn --- B1626323
One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798
Email: 510*/www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003786: arm:2R [607836,924593] estimated-cyto:41F5-41F9: 08/23/2001
Plate: RH.670 row: A column: 6
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                                                                                                                         BDGP
Lawrence Berkeley National Lab
Berkeley, CA
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152 c 180 g 124 t 1 others
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/lab_host="DH5-alpha TonA"
/clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
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/mol type="mRNA"
/db xref="texon:7227"
/clone="RH22614"
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                                                                                                                                                          Plate: 136 row: L column:
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                 Contact: Cameron, RA, Davidson, EH
Division of Biology 156-29
California Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                             Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ208101 936 bp DNA linear GSS 31-AUG-2000 SP_0136_B1_F01_T7A Strongylocentrotus purpuratus, purple sea urchin , sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=136 Col=1 Row=L, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                   additional resources
Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                       Email: acameron@caltech.edu
                                                                                                                                                                                                                                                       Pasadena California 91125, USA
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                                                                                                                         quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                        (626) 395-8421
(626) 793-3047
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Location/Qualifiers
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        /organism="Strongylocentrotus purpuratus"
/mol type="genomic DNA"
/db_xref="taxon:7668"
/clone="Plate=136 Col=1 Row=L"
/clone_lib="Strongylocentrotus purpuratus, purple sea
/rclone_spendence BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

163 c 198 g 133 t 1 others
 /note="Organ:
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/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/clone_lib="RH Drosophila melanogaster normalized Head
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/db_xref="taxon:7227"
/clone="RH67006"
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/mol_type="mRNA"
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Pred. No. 27;
sperm; Vector: BACe3.6; BAC Clones in E-Coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              BF307868 1083 DP WIND CONE 601890683F1 NIH_MGC_17 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                           mRNA sequence.
BF307868
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN17C24 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                       BF307868.1
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                                                                Homo sapiens (human)
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/note="end: T7"
287 c 249 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DN
/db_xref="taxon:7227"
/clone="BACN17C24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="DrosBAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Drosophila melanogaster"
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                                                                                                       GI:11255033
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CNSOOATX
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marmonser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS00ATX 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR22L05 of RPCI-98 library from Drosophila melanogaster (fruit
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Tissue Procurement: ATCC
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Drosophila melanogaster
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GSS.
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plate: LLCM1030 row: e column: 21
High quality sequence stop: 466.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db xref="taxon:9606"
/clone="IMAGE:4131836"
/tissue_type="rhabdomyosarcoma"

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence T7 end of BAC BACN12F17 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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AL104246.1 GI:5615857
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/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACR22L05"
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/note="end : T7"
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Tyler, B.M., Judelson, H.S., Gijzen, M., E
USDA-IFAFS: Expression of Phytophthora
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids 1; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 343)
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CD262900.1 GI:31050727
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Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Plate: 019
                                                  Email: bmtyler@vt.edu
                                                                1880 Pratt Dr., Blacksburg,
Tel: 540-231-7318
                                                                                                                    Tyler lab
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                                                                                                                                                                                                                                                                                     Phytophthora sojae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlerao, R., Jansson, S. Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI123995.1 GI:18007970
                   FORWARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene expression in Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1033P32P Populus leaf cDNA library Populus tremula x Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lundeberg, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus tremula x Populus tremuloides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCTCATCGCTCTCGT 32
                                PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rikerl@biochem.kth.se.
Location/Qualifiers
                                                                                                                                    Tyler B
                BK reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Populus tremula x Populus tremuloides"
|mol_type="mRNA"
|/mol_type="mRNA"
|/db_xref="taxon:47664"
|/clone_ilb="Populus leaf cDNA library"
|/note="Organ: leaf"
|89 c 58 g 121 t
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row: K
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10
                                                                                  VA 24061, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 343; 80;
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                                                                                                                                                                                and Waugh, M.E.
nes during infection
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BY076213/c
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VERSION
KEYWORDS
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MEDLINE
PUBMED
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                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                              Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Nikado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldareili, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schimil, L.M., Kanapin, A., Matsuda, H., Batalov, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gastberland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numara, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Raid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sutana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Wang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Yang, L., Yang, L., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Azakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, D., Sato, C., Sato, R., Lander, C., Sato, S., S
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Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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BY076213 RIKEN full-length enriched, pooled tissues, adult etc. Mus musculus cDNA clone K630003D15 5', mRNA sequence.
                           Laboratory for Genome
                                                         Contact: Yoshihide Hayashizaki
                                                                                                                        22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okazaki, Y., Furuno, M., Kasukawa, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: BK reverse High quality sequence
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/mol_type="mRNA"
/db_xref="taxon:67593"
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125 c 106 g 55 t
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cell_line="P6497"
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81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi, J.,
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                        RIKEN Genomic
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RESULT 28
AU029704/c
                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,
Aizawa,K., Akimura,T., Arakawa,T., Cawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Makai,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
AU029704 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E31310_6Z, mRNA sequence.
AU029704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:10090"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                   32.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _lib="RIKEN full-length enriched, pooled tissues,
spleen, etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ი
                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 404)
                                                                                                                                                                                                Elanco Animal Health, A Division of Eli Lill
PO Box 708, 2001 West Main St., Greenfield,
Tel: 317 277 0826
Fax: 317 277 4522
                                                                                                                                                                                                                                                Contact: Hill CA
Animal Science Discovery Research
Animal Health, A Division of Eli Lilly and Company
Greenfield, IN 46140, USA
                                                                                                                                                                                                                                                                                                                                                            Microb. Comp. Genomics 5 (2), 89-101 (2000) In press Contact: Hill CA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hill,C.A and Gutierrez,J.A.

Analysis of the expressed genome of the lone star tick, americanum (Acari:Ixodidae) using an expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            americanum cDNA, mRNA sequence. BF008574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF008574 406 bp mRNA linear EST 06-OCT-
1613456 Amblyomma americanum larva Lambda Zap Express Amblyomma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                      approach
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1 (bases 1 to 406)
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Parasitiformes; Ixodida; Ixodidae; Amblyomma.
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/clone_lib="Rice panicle shorter than 3cm"
/note="Organ: panicle"
89 c 125 g 97 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                /mol_type="mRNA"
/db_xref="taxon:6943"
                                                                          'organism≐"Amblyomma americanum"
                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                     CATHERINE_A@LILLY.COM
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Length 404;

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EST 06-OCT-2000

Amblyomma

cultivar-group) "

Tsukuba, Ibaraki

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SOURCE
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Matches 17
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Email: h-lewin@uiuc.edu

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

Form Washington University Genome Center PHRAP suite.

Sequences submitted are vector free and at least 200 bp in length.
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BACKWARD: ATTAACCCTCACTAAGG
Insert Length: 425 Std Error: 0.00
Plate: BP230018B10 row: F column: 10
Seq primer: AGCGGATAACAATTCACACAGGA
High quality sequence stop: 425.
Location/Qualifiers
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University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW465276
AW465276.1 GI:7035444
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished Contact: Lewin, H. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
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BP230018B10F10 Soares normalized bovine placenta Bos taurus cDNA
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                                                                  /note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI; The CDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                lab_host="DH10B"
                                                                                                                                                                                                                                                                        clone="BP230018B10F10"
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/clone_lib="Amblyomma americanum larva Lambda Zap Express"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
/note="Vector: pBK-CMV; Site_1: A others
                                                                                                                                                                                                                                                        sex="female"
  32.7%;
100.0%;
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100.0%;
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83;
DB 9;
84;
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                 Length 425
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DEFINITION
ACCESSION
VERSION
                                                                                                            RESULT 32
AW376507/c
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Best Local Similarity
Watches 17; Conserve
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AUTHORS
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                                             IL3-CT0213-161299-038-F12
AW376507
AW376507.1 GI:6881168
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AMO56R2:
Homo sapiens (human)
                                                                                            AW376507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; 1 (bases 1 to 446) Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R. The Pine Gene Discovery Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Minnesota.
Seq primer: 5' lambda TriplEx2 Sequencing Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rosswhet@unity.ncsu.edu
Shoot tip library plates ST01-ST50 were prepared and sequenced
NCSU. Plates ST51-ST99 were prepared and sequenced at IFG/CSUH.
Informatics was done at the Computational Biology Centers (CBC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus taeda (loblolly pine)
Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 919-515-7800
Fax: 919-515-7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Ross Whetten
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                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli BM25.8"
/clone lib="pine TriplEx shoot tip library"
/clone lib="pine TriplEx shoot tips (approx. 2 cm from the speak were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:3352"
/clone="ST56F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Pinus taeda"
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ATCGCTCTCGTCGCTGC 38
                                 Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                             i (bases 1 to 490)
Anderson,O.D., Chao,S., Choi,D.w., Clc,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Seaton,C.L. and Tong,J.C.
The structure and function of the expr
                                                                                                                                                                                                                                                                                                                                                    BQ170403 490 bp mRNA linear EST WHE1770 E05 J10ZT Wheat pre-anthesis spike cDNA library sectioum cDNA clone WHE1770_E05_J10, mRNA sequence. BQ170403 BQ170403.1 GI:20332226 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0213-
161299-038-F12&t3=1999-12-16&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
                                                                                                                            Genomes - P
Unpublished
                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Tracheonideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brazil
Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   Fax: 5105595818
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oandersn@pw.usda.gov
                                                                                                                                        ucture and function of the expressed portion - Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196: 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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345 CTCTCGTCGCTGCCGGC 361
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Analysis of bovine mammary gland EST and the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 505)
Sonstegard, T., Capuco, A.V., White, J., V., Cho, J., Sultana, R., Shade, L., Wray, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This EST was generated by sequencing from the 3' end of the Sequences have been trimmed to remove vector sequence and lo quality sequence with phred score less than 20. Seq primer: T7 primer.
                    Plate: 135 row: J column: 12
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                and -minmatch 12 options.
PCR PRimers
                                                                                                                                                        Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                 Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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17; Conserv
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Fax: 301 504 8414
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                                                                   BACKWARD: GTTTTCCCAGTCACGACG
                                                                                            FORWARD: AGGAAACAGCTATGACCAT
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/db_xref="taxon:465"
/clone="WHE1770_E05_J10"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone lib="Wheat pre-anthesis spike cDNA library"
/clone lib="Wheat pre-anthesis spike cDNA library"
/clone: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
Location/Qualifiers
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/cultivar="Chinese
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100.0%; Pr
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0; Mismatches
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J.E., Wells,K.D. a
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  Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefeb, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii Eukaryota; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ821431 506 bp mRNA linear EST 01-AUG-2002 1030092C04.yl C. reinhardtii CC-1690, Deflagellation (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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BQ821431.1 GI:22072093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Charles Hauser
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                                                    /mol_type="mkNA"

/mol_type="mkNA"

/strāin="CC-1690 wild type mt+ 21gr"

/db_xref="taxon:3055"

/clone lib="c. reinhardtii CC-1690, Deflagellation

/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:

/mol_te="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:

XhoI; Deflagellation library, constructed by John Davies

and Jeffrey McDermott, combines cDNAs from CC-1690 cells

which had been re-synthesizing flagella for 15, 30 and 60

min after being deflagellated by pH shock. PolyA mRNA was

purified from each sample, pooled and cDNA synthesized.

The cDNA was directionally cloned into lambda Zap II

(Stratagene) in the EcoRI (5') and xhoRI (3') sites.

pBluescript II SK- plasmids were excised from the lambda

ZAP clones by superinfection with ExAssist (Stratagene)

phage. The library was normalized using method 4 described

in Bonaldo et al., (1996) Genome Research 6: 791-806."
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/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Chlamydomonas reinhardtii"
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/lab_host="DH10B"
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87;
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AI988643/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 call: (800)-533-4363 or contact via
Insert Length: 810 Std Error: 0.00
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., and Wilson, R.
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Glycine max (soybean)

Glycine max
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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               /clone lib="Gm-cl020"
/clone lib="Gm-cl020"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from nodules on the roots of 2.5 month-old Glycine max
/williams' plants that were greenhouse grown. The The CDNA
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. First strand synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (v=A, C, or G) was added to the 3' end of the
primer [GACAGAGAGAGAGAGAGACTACTCTCGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase and size- fractionated with a
400 bp cutoff, using a SizeSep 400 Spun column from
Pharmacia. The column eluent was ligated to EcoR1 adaptors
and phosphporylated. The XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size- fractionated with a 500 bp cutoff,
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/db xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl020-850"
/tissue type="root nodules of greenhouse grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Glycine max"
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GibcoBRL Life Technologies' cDNA Size Predigested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Std Error: 0.00
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Beck, C.,
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REFERENCE
AUTHORS
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AV668034/c
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ORIGIN
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ORIGIN
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Best Local S
Matches 17
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Best Local S
Matches 17
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MEDLINE
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                                                                                                                                                                                                                                                                                                                         source
                                 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV668034
AV668034 Bos taurus ova.
5', mRNA sequence.
AV668034
AV668034.1 GI:9932779
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 TCTCATCGCTCTCGTCG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                      Single pass sequencing.
This clone was obtained from a polyA-deleted
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                         . Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           poly(A) tai
bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 29
                                                  ATCGCTCTCGTCGCTGC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTCATCGCTCTCGTCG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugimoto, Y.
                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lishment of a high throughput EST sequencing system using a) tail-removed cDNA libraries and determination of 36,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=56) and sequence (n=16). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryary was constructed by Dr. Paul Keim and Dr. Virginia Coryary 1 others
                                                                                                                                                                            was
                                                                                                                                                          /clone libb "Bos taurus ovary fetus"
/note="Vector: pZL1; Site_1: Sal1;
was deleted from a Not1 site"
153 c 187 g 81 t
                                                                                                                                                                                                                  /tissue_type="ovary"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                /clone="E10V019D09"
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                                                                                                    32.7%;
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Pred. No.
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Pred. No.
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88;
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88
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                                                                                       Indels
                                                                                                                                                                                       Site_2: Not1; Poly
                                                                                                                                                                                                                                                                                                                                                     cDNA library.
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                REFERENCE
AUTHORS
                                                                                                                                                                                     RESULT 39
AV597173/c
LOCUS
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VERSION
KEYWORDS
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AI542489/c
                                                                                                                VERSION
KEYWORDS
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Best Local (
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1 (bases 1 to 546)
Takasuga, A., Hirotsune, S.,
and Sugimoto, Y.
                                                                                   Bos taurus
                                                                                                  Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI542489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                     Conservative
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AI542489 544 bp mRNA linear EST 21-APR-2001 SD08831. Sprime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD08831 5 similar to AJ010298: Drosophila melanogaster retrotransposon-like element,
                                                                                                                                                                                                  AV597173 Bos taurus cartilage EICA030D01 5', mRNA sequence. AV597173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dase 1 to 544)

1 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, Lewis, S., and Rubin, G.M.
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: SD.88 row: C column: 7 High quality sequence stop: 459 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003350: arm:U [4635408,4651408] estimated-cyto:?:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
on Mar 19, 1999 this sequence version
Other ESTs: SD08831.3prime
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                             AV597173.1 GI:9714516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI542489.2 GI:13771703
                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
Core Corolotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pOT2; Site 1: EcoRI; Site 2: Xho1; Sized fractionated CDNAs were directly ligated into pOT2. Plasmid cDNA library."

a 148 c 171 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="SD Drosophila culture pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="prosophila melanogaster"
|mal_type="mRNA"
/db xref="taxon:7227"
/clone="SD08831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH5-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17;
Pred. No.
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Itoh, R.,
                                                                                                                                                                                                                                            e fetus
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88
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                                                                                                                                                                                                                                                                    mRNA
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Jitohzono,
                                                                                                                                                                                                                                            Bos taurus cDNA clone
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Suzuki, H.,
                                                                                  Euteleostomi;
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ACCESSION
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LOCUS
DEFINITION
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MEDLINE
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Jap.
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                     Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                         Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV603191 556 bp mRNA linear EST 27-NOV-2001
AV603191 Bos taurus kidney fetus Bos taurus cDNA clone E1KI014F12
5', mRNA sequence.
AV603191
                                                                                                                                                                                                              Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                   Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                       Establ
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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EST.
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                                                                                                                                                                                                                                                                                    bovine ESTs
                                                                                                                                                                                                                                                                                                   Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 29 (22), E108 (2001)
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                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 556)
                                                                                                                                                                                                                                                                                                                                        Sugimoto, Y.
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1. .556
/organism="Bos taurus"
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was deleted from a Not1 site"
148 c 180 g 89 t 3 others
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/db_xref="taxon:9913"
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359 ATCGCTCTCGTCGCTGC 343
                         22 ATCGCTCTCGTCGCTGC 38
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17; Conservative
                                                                                                                     127
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was deleted from a Not1 site"
150 c 187 g 89 t 3 others
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100.0%; Pred. No. 89,
tive 0; Mismatches
                                                                DB 9;
89;
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Search completed: November 13, 2003, 10:59:31
Job time: 2025 secs

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-DB=N_Geneseq_19Jun03_-OFMT=fastap_-SUFFIX=rng_-MINMATCH=0.1 -LOOFCL=0
-LOOFEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45_-DOCALICUS=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -LIGN=40
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-NGAP -LARGEQUERY_NEG_SCORES=0 -MATT -DSUBLOCK=100 -LOUGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
                            November 13, 2003, 10:59:37; Search time 218 Seconds (without alignments) 222.889 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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82
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA199.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:
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SUMMARIES

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;	Human ORF	24-JUN-20	ABN20845;	B 4	D F-1		. 4	4.4	. 4.	4.4	.	4.4	.4.	42	4.4	2.4	4.	י בי	4.4	44	. 4.	44	44	4. 4	44	. 4.	44	٠ 4.				. 4.	5 46		2 47	Scor	ď									
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	quence SEQ ID NO:1016			BP.		ALIGNMENTS	AAA95409	ABQ79598	ABQ79595	ABQ79597	AAQ58018 ABO79594	AAQ58017	ABO79601	ABQ79602	ABQ79607	ABQ79606	ABQ79615	AAS85360	3816	AAF21610 AAA81490	AAF21609	AAS87868	ABL50562	ABL03546	ABZ66799 AAS90583	AAC95143	AAV69642	ABL12108	ABL17906	ABL17909	ABL12109 ABL17907	ABI99479	9968 9289	AA199683	ABN20845 AAS59592	D		SUMMARIES								
	7.						Trichoderma reesei	. reesei cbhl ge	. reesei cbhl	cbh1 ge	Sequence of altere	Sequence of altere	Drosophila melanog T. reesei cbhl gen	T. reesei cbhl gen	T. reesei chhi gen	DNA encoding novel T. reesei cbh1 gen	T. reesei cbhl gen	Staphylococcus epi	S. epidermidis ope	Neisseria meningit N. meningitidis B	Neisseria meningit	DNA encoding novel	Micromonospora car	Drosophila melanog	Orthosomycin biosy DNA encoding novel	lea hea	ophila fat fa flee head and	ophila melano	Drosophila melanog	rosophila melano	rosophila melano	ouse ischaemic c	Mycobacterium tub NA encoding novel	obacterium tu	ORFX onibac	scription										

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                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences can be used in gene therapy. OREX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000;
29-AUG-2000;
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AAS59592
                               AAS59592 standard; DNA; 5888
                                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                  Sequence 450
                                                                                                                                                                                                                                                                                                                                                                                                N.B. The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 10167; 1037pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                   GCTCTCATTGCCCTGGTGGCTGGCCTGGCCTTCA 181
                                                                                                                         AlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
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2000US-228716P.
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                                                                                                                                                                                                                                                                                                  CC Propionibacterium acnes immunogenic polypeptides. The proteins and their C associated DNA sequences are used in the treatment, prevention and CC diagnosis of medical conditions caused by P. acnes. The disorders include CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and storders include CC in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne could be contral metrous associated with acne in a CC patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein CC in the sample. The polypeptides may be used as antigens in the production CC in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and CC therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by cenzyme linked immunosorbent assay (ELISA). This sequence encodes the CC Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAS59506-AAS59804 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW, Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001;
                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                      specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-616774/71.
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; 2000US-208841P.
; 2000US-216747P.
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, Jen S, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the sequences of M. tuberculosis strains CDC 1551 (AAI99683) and nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and HJ7Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4411529 BP; 758565 A; 1449983 C;
                                                                     DNA encoding novel human diagnostic protein #20093
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                             Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic c
                                                                                                                                                              standard;
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of.

Homo sapiens

Query Match:

Similarity:

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Percent Similarity: Best Local Similari

Sequence 1947 Bp;

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from

547 A; 520 C; 485 G; 395 T; 0

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The invention relates to an isolated nucleic acid detection reagent useful in developmental biology and in elucidating cell signalling insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL)6175) and the encoded proteins for invention and (ABBS7737-ABB72072).

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Claim 1; SEQ ID NO 5200; 21pp + Sequence Listing; English.

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The invention relates to an isolated nucleic acid detection reagent useful in developmental biology and in elucidating Call Signalling insecticides, therapeutics and pharmaceutical drugs. The invention listcloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                             Claim 1; SEQ ID NO 5191; 21pp + Sequence Listing; English.
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genes from Drosophila and
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 5191.
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                                                                                                            detection reagent for detecting for elucidating cell signalling
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Sequence 4754 BP; 1313 A; 1004 C; 980 G; 1457
       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                 The invention relates to an isolated nucleic acid detection reagent useful in developmental biology and in elucidating cell signalling (insectice), therapeutics and pharmaceutical drugs. The inventificationses genomic DNA sequences (ABL16176-ABL30511), expressed DNA 1857737-ABB72072).
                                                                                                                      Claim 1; SEQ ID NO 5197; 21pp + Sequence Listing; English.
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genes from Drosophila and
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 30806; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABB68005.
                                                                                                                                                                                                                                        Sequence 4790 BP; 1324 A; 1012 C; 986 G; 1468 T; 0 other;
                                                                                                                                                                                                                                                                                                                  specification,
                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                 sequence data for this patent did not form part oscification, but was obtained in electronic format ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla
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Conservative:
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                                                                                                                                                                                                                                                                This represents the nucleotide sequence of Drosophila fat facets related Y (DFFRY) gene. The invention relates to genes occurring on the non-recombining region of the human Y chromosome. The sequences fall into two classes (1) X-homologous DNA which are expressed in many organs, having functional X homologues and (2) testis-specific DNA sequences. Y chromosomal DNA from males with known conditions such as sequences. Y chromosomal DNA from males with known conditions such infertility and reduced sperm count can be assessed using the invention to determine whether the condition is associated with or caused by the occurrence of the gene or gene alteration. Candidate inhibitors of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene alteration; DFFRY; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-recombining region; human; Y chromosome; X homologue; testis; infertility; sperm; Drosophila fat facets related Y; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila fat facets related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV69642 standard; DNA; 10091 BP
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                                                                                                                                                                                                                                                        enzymatic activity of the genes can be assessed using
                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 7A-D; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel genes in the non-combining region diagnose if male infertility or reduced
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                                                                                                                                                                                                                               Sequence 10091 BP; 3208 A; 1797 C; 2103 G; 2983 T; 0 other;
           AAC94394 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page DC;
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  US-10-081-935-2 (1-18)
                                                                                                                                                                                                                                                            CC constructs, recombinant virtues and recombinant cells comparising the controlled acids of the invention, recombinant production of the proteins, cantibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for compositions compositions the inhibitors for controlled acids, and the proteins they concole may be used in the prevention, treatment and diagnosis of diseases considered with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant collective collecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cat flea; head and nerve cord nucleic acid; HNC; flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis; detection; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flea Malpighian tubule and head acids useful for the prevention,
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                                                                                                                                                          No. :
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The invention relates to novel cat flea (Ctenocephalides felis) nucleic CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue CC or head and nerve cord (HNC) tissue. The invention also relates to the CC encoded proteins. The invention additionally encompasses expression CC constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, and compositions comprising the inhibitors for CC antibodies against the proteins, a method of identifying inhibitors of CC administration to an animal. The nucleic acids, and the proteins they CC encode may be used in the prevention, treatment and diagnosis of diseases CC used to produce an HMT or HNC protein according to standard recombinant CC DNA methodology by inserting the nucleic acids into a host cell and CC culturing the cell to express the protein. The HMT and HNC nucleic acids cand quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and CC function of the proteins and their role in metabolism. The HMT and HNC protein may be used as antigens in the production of specific contibodies, and in assays to identify modulators (agonists and the CC antibodies, and in assays to identify modulators (agonists and CC antibodies, and in assays to identify modulators (agonists and CC antibodies, and in assays to identify modulators (agonists and CC antibodies, and in assays to identify. The antibodies may also be used to samples (e.g., by enzyment) inked immunosorbent assay (ELISA)). The content assay (ELISA). The protein expression and activity. The antibodies may also be used in samples (e.g., by enzyment) inked immunosorbent assay (ELISA). The content assay (ELISA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
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                                     , by enzyme linked immunosorbent assay represents a cat flea HNC cDNA of the
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                                                                                                               Percent Similarity:
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                                                                                                                                                                         Alignment Scores
                                                                                                                                                                                                                                         The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ666813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABP99207-ABP99362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene cluster. The method is useful for detecting the presence of any organism that contains DNA for the production of envinosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orthosomycin biosynthetic polynucleotide SEQ ID NO 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthosomycin; biosynthesis; everninomicin; avilamycin; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ66799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying orthosomycin biosynthetic gene, cluster, by detecting presence of nucleic ac to 17 of flambamycins protein families -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001US-279095P.
30-MAR-2001; 2001US-279709P.
20-APR-2001; 2001US-285214P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micromonospora carbonacea africana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2002; 2002WO-CA00432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 409; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058435/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farnet CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ECOP-)
                                                                                                                                                                                                    Sequence 1554
                                                                                                                                                                                                                               orthosomycin natural products, not produced by the organism
                                                                                                                                                           NO. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECOPIA BIOSCIENCES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
                        MetGlnPheSerHisAlaLeuIleAla-----
ATGAGACATCGTCATGCCCTGCTGGCCGTCGGCACCACCGCGACCCTGGTCGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zazopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                      BP; 267 A; 615 C; 474 G; 198 T;
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                                                                                      326
43.00
63.64*
54.55*
52.44*
                                                         ABZ66799
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                                                           (1-1554)
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Matches:
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acid sequence corresponding
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                -----LeuValAlaAlaGly 14
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RESULT 17
RAS90583
ID AAS90583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC polypeptide (II) sequences. (I) is useful as hybridisation probes.

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome complexes are also used in diagnostics of (II). The complexes are also used in diagnostics as expressed sequence tags complexes are also used in diagnostics as expressed sequence tags complexes are also used in diagnostics as expressed sequence tags complexes are to treat disease states involving complexes are trivity of (II) or to treat disease states involving complexes are polypeptide in tissue, as molecular weight markers and as complexes are useful for treating or complexes are expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating complexes involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in composition of the expression of mutations in the printed composition of the expression of mutations in composition of the expression of mutations in composition of the expression of mutations in the printed composition of the expression of mutations in composition of the expression of mutations in the printed composition of the expression of mutations in the printed composition of the expression of the invention.

CC note: The sequence and products dependent on DNA and composition of the expression of the invention of the expression of mutations in the 
                                                                                                                                                                                                                                                                                      Alignment Scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
P-PSDB; ABG26396.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 26387; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and
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upplement; medical in
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2000US-0649167.
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379
43.00
80.00%
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52.44%
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                                                                                                                                                                                                                                                                                                                                                                                                 368 C;
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maging; diagnostic; genetic disorder; ss.
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                                                                                                                                             Length:
Matches:
Conservative:
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Query Match: DB:

Best Local Similarity:

Mismatches: Indels:

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Percent Similarity:
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                                                                            US-10-081-935-2 (1-18) x ABL03546 (1-6783)
RESULT 19
                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL6176-ABL30511), expressed DNA sequences (ABL6175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                  Sequence 6783 BP;
                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5120; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions
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                        TTTTCGAATCTTCTATTAACACTACTTGTCGCAGGATTGGCTTCT 6033
                                        PheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
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43.00
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ABZ66813/c

ID ABZ66813 standard; DNA; 10035 BP.

XX AC ABZ66813;

XX 21-MAR-2003 (first entry)

XX Orthosomycin biosynthetic gene clus

XX Orthosomycin; biosynthesis; evernin

XX 28-MAR-2002; 2002WO-CA00432. .

XX 28-MAR-2001; 2001US-279095P.

XX 28-MAR-2001; 2001US-279095P.

XX 28-MAR-2001; 2001US-27909P.

XX 28-MAR-2001; 2001US-285214P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ666813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABP99207-ABP99362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene fragment of gene cluster. He method is useful for detecting the presence of any organism that contains DNA for the production of orthosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin produced by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new orthosomycin natural products, not produced by the organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying orthosomycin biosynthetic gene, cluster, by detecting presence of nucleic ac to 17 of flambamycins protein families -
                             ABL50562 standard; DNA; 11115 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10035 BP; 1396 A; 3516 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 506-511; 511pp; English.
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RESULT 21
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                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                  carbonacea everninomicin biosynthetic locus gene cluster. The contigs encode the protein sequences designated ORF (open reading frame) 1 to 49, given in ABB06881 to ABB06330. The gene cluster is useful for the construction of the everninomicin antibiotic in overproducing strains, and to allow chemical modifications of everninomicin to enhance certain properties via genetic manipulation or combinational biosynthesis. The gene cluster can be used to produce genetic systems and genes encoding novel enzyme activities, and avoid the problems of low yield and quality of everninomicine arroduced by chemical protects.
    13-FEB-2002
                          AAS87868;
                                             AAS87868
                                                                                                                                                                                                                                                                                       Sequence 11115 BP; 1521 A; 3924 C; 4057 G; 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Micromonospora carbonacea; antibiotic; everninomicin; biosynthesis; gene cluster; genetic manipulation; contig; gene; ds.
                                                                                                                                                                                                                                                         NO::
                                                                                                                                                                                                                                                                                                                                                                                                  ABL50555 to ABL50562 represent contigs 1 to 8 from the Micromonospora carbonacea everninomicin biosynthetic locus gene cluster. The contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated gene cluster encoding polypeptides involved in everninomicin biosynthesis useful for construction of everninomicin overproducing strains, and to allow chemical modifications of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB06928,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476185/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staffa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2001; 2001WO-CA00128
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                                                                                                                                                                                                                                                                                                             everninomicins produced by chemical synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOPIA BIOSCIENCES INC FARNET C.
                                             standard; cDNA; 11220 BP
                                                                                         CTGGCC 7759
                                                                                                            LeuAla 16
                                                                                                                                                       MetGlnPheSerHisAlaLeuIleAla----
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   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      to enhance certain properties
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RESULT 22
AAA81459/c.
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                                                                                            US-10-081-935-2 (1-18) x AAS87868
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Best Local Similarity:
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7210

standard; DNA; 56609 BP

(1-11220)

80.00% 53.33% 52.44% 23 43.00 3.66e+03

84400

Length: Matches: Mismatches: Indels: Conservative:

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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC can dentifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC disgnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed confictation, but was obtained in electronic format directly from WIPO care from vino int/min/inshed are resonences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, forensics, responsible for genetic biodiversity -
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Sequence 11220 BP; 4082 A; 2495 C; 2204 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 23672; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
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                                                                                     ftp.wipo.int/pub/published_pct_sequences.
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    T; 2 other;
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Best Local Similarity: Query Match:
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                                                    Percent Similarity:
                                                                                                                                                                                      represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB2563 represent the Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81259 and AAA81324 to AAA81325 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism specific probes. Attempts to make efficacious Meningococcus B vaccines have falled mainly due to antigen tolerance. Weningococcus B vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frazer CM, n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleotide sequences of Neisseria meningitidis which carused in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis partial DNA sequence gnm_7 SEQ ID NO:7.
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30-APR-1999;
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Galeotti C, Mora M,
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99US-0132068
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Ratti G, Scarselli M,
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   Percent Similarity:
                                                                                   Alignment Scores
                                                                                                                                                                                                                         CC to AAF21613 mentions for the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 cc sequences which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC Neisseria proteins given in AAB88550 to AAB85593, and AAF21589 to CC AAF21606 represent PCR primers which are used in the exemplification of CC the present invention. The NMB genome and fragments from it have CC maintibacterial activity, and can be used in vaccines and gene therapy. CC Neisseria nucleic acids, proteins and/or antibodies which binds to the CC proteins can be used in compositions for treating or preventing infection CC due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial bacteria or as earch to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
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Galeotti C,
                                                                                                                                                  Sequence 349980
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08-OCT-1999;
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C, Mora M,
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Ratti G,
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Scarselli M,
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Matches:
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                                                                                                                                                  95584
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Scarlato V,
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Rappuoli R;
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CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 CC sequences which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21547 is repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21507 are repeated at CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to CC AAF21606 represent PCR primers which are used in the exemplification of CC the present invention. The NMB genome and fragments from it have CC antibacterial activity, and can be used in vaccines and gene therapy. CC Neisseria nucleic acids, proteins and/or antibodies which binds to the CC proteins can be used in compositions for treating or preventing infection CC due to Neisserial bacteria or as a diagnostic reagent for detecting the CC proteins. Computers, computer storage medium or computer CC databases can be used in a search to identify open reading frames (ORFs) CC or coding sequences within the NMB genome. The DNA sequences provide CC used effective in vaccines than the outer membrane proteins which are CC used.
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28-FEB-2000; 2000GB-0004695
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C, Mora M,
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99WO-US23573.
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Ratti G, Scarselli M,
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Scarlato V,
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RESULT 25
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AAAB1452 represent Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes, and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism specific probes. Attempts to make efficacions
                                                                                                                                                                                                        The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neismed meningitidis genomic DNA sequences, AAA81260 to AAA81103 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins, AAA81254 AAA81259 and AAA81314 to AAA81321 represent PCR primers used in the
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                                                                                                                                                                                                                                                                                                                                                         Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                             Claim 7; Page 866-1272; 1760pp; English.
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99US-0132068
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92.31%
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C, Mora
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Ratti G, Scarselli M,
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AAH53816/c
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       AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
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                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                 Nucleic acids encoding useful for vaccinating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccination;
                                                                                                                                                                                                                                                                                                                                                                     (GLAX )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermidis
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DB; AAG82966.
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                                                                                                                                                                                                                                                                                                                                                                     GLAXO
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represent oligonucleotide sequences and primers
                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTTGCTCATTCTGATTGCTGCGGGTCTCGCTGCGGCT 1187702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us epidermidis SR1 endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                       796-797;
                                                                                                                                                                                                                                                                                                                                                                     GROUP
                                                                                                                                                                                                                                                                                                                                                                                                 99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        open reading
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43.00
92.31%
69.23%
52.44%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                              polypeptides from Staphylococcus epidermidis,
                                                                                                                                                                                                                     2188pp;
                                                                                                                                                                                                                                                 against infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame nucleotide sequence SEQ ID NO:3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain;
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection;
                                                                                                                                                                                                                                                 e.g. endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1437668
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis
 which
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are used
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment
                                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABp35124 to ABp37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 44 no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                     Disclosure; SEQ ID 959; 267pp;
                                                                                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                      14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN91496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6380370-B1
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                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATTTTCACATTCTCTTCTACGTCTAATCGCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1-18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                          THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                   97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis ORF nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                             98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 A;
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42.00
82.35%
58.82%
51.22%
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                                                                                                                                                                                     English.
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                             treating bacterial infections
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10
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Sequence 504 BP; 188

Α, 61 C;

114 G;

141 T; 0 other

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Query
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AAS85360/c
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Pred. No.:
     CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore mormal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating annibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. (C The polypeptide and polynucleotide sequences have applications in CC diagnostics forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fery whos, int/bub/sublished pot sequences.
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                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #21164
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ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                     invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID No 21164; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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Matches:
Conservative:
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Indels:
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Alignment
Pred. No.:
             Percent Similarity:
Best Local Similari
Query Match:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                           The invention relates to a DNA sequence located in a promoter of a secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cbhl gene promoter. The promoters of the invention are modified such that they lack the present sequence.
                                                                                                                                                                                                                                                                                                                      Pakula T,
Jeenes D,
                                                                                                                                                                                                                                                 New DNA sequence located in a promoter of a secretable protein, useful for optimized protein production and design better fungal strains for protein production .
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                                                                                         Sequence 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200264624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichoderma reesei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T. reesei cbhl gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ79615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ79615 standard;
                                                                                                                                                                                                                            Disclosure; Page 84; 84pp; English.
                                                                                                                                                                                                                                                                                                WPI; 2002-657583/70
                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001FI-0000272
                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002; 2002WO-FI00116
                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; transcription; secretion stress; fungal; cbhl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                       (VALW ) VALTION TEKNILLINEN TUTKIMUSKESKUS
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                                                                                                                                                                                                                                                                                                                      Archer D,
                                                                                                                                                                                                                                                                                                                                Saloheimo M,
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                                                                                         256 A;
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42.00
84.62%
53.85%
51.22%
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42.00
78.57%
64.29%
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Penttilae M;
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                                 Matches:
Conservative:
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Similarity:

Mismatches: Indels:

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Alignment
Pred. No.:
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AAS83866/c
                                                                                                                                                CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating annibodies against it, detecting or CC (III). (II) is useful for generating annibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC are fell wino in fully hyphilable for temperature.
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                Percent Similarity:
 Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 19670; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG19679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                     NO . .
                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73
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                                                                                                      ВP;
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                                                                                                      257
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42.00
82.35%
47.06%
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                                                                                                    302 G; 163 T;
              Length:
Matches:
Conservative:
 Mismatches:
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                                                                                                      other;
951
3
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ABQ79607/
ID ABQ7
                         RESULT 32
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                                                                                                  US-10-081-935-2 (1-18) x ABQ79606 (1-1031)
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                                                                                                                                                                             Score:
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                                                                                                                                                                                                                                                 The invention relates to a DNA sequence located in a promoter of a secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cbh1 gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                         for optimized protein production and design better fungal strains for protein production \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pakula
Jeenes
                                                                                                                                                                                                                             Sequence 1031 BP;
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 81; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein;
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00 GAGTTCTCACAAGATCTGATGGTTTTATTAGCGTCTGGCATTTCTTCTGCT
                                                                      PheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeu
                                               TTTAGCCACTTGATTGTACAATTATTAGCCGCTGGTATA
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Archer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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42.00
84.62$
53.85$
51.22$
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23
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Conservative:
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ABQ79607

standard;

DNA; 1201

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RESULT 33
ABQ79605/C
ID ABQ77
XX ABQ79
AC ABQ79
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DB:
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Best Local Similarity:
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Jeenes D,
                     Trichoderma reesei.
                                                                                                                                                                                                        25-NOV-2002
                                                                                                                                                                                                                                                                                                             ABQ79605 standard; DNA; 1281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA sequence located in a promoter of a secretable protein, useful for optimized protein production and design better fungal strains for protein production -
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                                                                                                                                                      cbh1
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Archer D, P
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53.85%
51.22%
24
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42.00
                                                                                                                                                   fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 C;
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                                                                                                  secretion
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Matches:
Conservative:
Mismatches:
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                                                                                               stress;
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                                                                                             fungal; cbh1;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pakula T,
Jeenes D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pakula T,
Jeenes D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cbhl gene promoter.
                                                                                                              22-AUG-2002
                                                                                                                                                             Trichoderma reesei
                                                                                                                                                                                    Secreted protein; transcription; promoter; ds.

    reesei cbhl gene fragment

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regulation of secreted proteins under secretion stress. The DNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 80; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA sequence located in a promoter of a secretable protein, useful for optimized protein production and design better fungal strains for protein production -
                                   (VALW ) VALTION TEKNILLINEN TUTKIMUSKESKUS
                                                            13-FEB-2001; 2001FI-0000272
                                                                                     13-FEB-2002; 2002WO-FI00116
                                                                                                                                     WO200264624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a DNA sequence located in a promoter of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001; 2001FI-0000272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002; 2002WO-FI00116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200264624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Match:
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                                                                                                                                                                                                                                                                                                                                              532
                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                             standard; DNA; 1474
                                                                                                                                                                                                                                                                                                                                                                   PheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                            TTTAGCCACTTGATTGTACAATTATTAGCCGCTGGTATA 494
Saloheimo M,
Archer D, Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saloheimo M,
Archer D, P
                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                             x ABQ79605
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42.00
84.62%
53.85%
51.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 A; 290
                                                                                                                                                                                                                                              entry)
   Penttilae

 Vusitalo J,
Penttilae M;

            Uusitalo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                             (1-1281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 317 G; 318
  3
                                                                                                                                                                                               secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
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            Huuskonen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huuskonen
                                                                                                                                                                                               atress;
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                                                                                                                                                                                              fungal;
             Watson
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            A
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a DNA sequence located in a promoter of a secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cobil gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1474 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA sequence located in a promoter of a secretable protein, useful for optimized protein production and design better fungal strains for
                                     Claim 1; SEQ ID NO
                                                                      genes from Drosophila
                                                                                                                                                                                              23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                pharmaceutical;
                                                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                       ABL02695;
                                                                                    New isolated nucleic
                                                                                                                                                                       (PEKE )
                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                         27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                              developmental
                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            x ABQ79602
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42.00
84.62$
53.85$
51.22$
                                     2567;
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a and
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                                                                                                                                                                                                                                                                                                                                 SS
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                                 21pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 C;
                                                                                                                                              PWD,
                                                                     detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                           biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-1474)
                                                                                                                                             Myers
                                  Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                             cell
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                                                                                                                                                                                                                                                                                                                                         signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1474
                                 English.
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                                                                      1000
and c
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invention

Sequence 1714 BP;

459 A; 389 C;

422 G;

444 T; 0 other;

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                 The invention relates to a DNA sequence located in a promoter of a secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cobhl gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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Jeenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutuical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                           New DNA sequence located in a for optimized protein product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                      Disclosure; Page 78; 84pp; English.
                                                                                                                                                                  protein
                                                                                                                                                                                                                    WPI; 2002-657583/70
                                                                                                                                                                                                                                                                                                                                                               22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein;

 T. reesei cbhl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ79601 standard;
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                                                                                                                                                                                                                                                                                   (VALW ) VALTION
                                                                                                                                                                                                                                                                                                           13-FEB-2001; 2001FI-0000272
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                                                                                                                                                                                                                                                                                                                                                                                         WO200264624-A2
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                                                                                                                                                                production
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                                                                                                                                                                                                                                           Saloheimo
Archer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                 TEKNILLINEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription; secretion stress; fungal; cbhl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
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42.00
91.67%
66.67%
51.22%
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment
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                                                                                                                                                                                                                                                         Ξ.
                                                                                                                                                                           ted in a promoter of a secretable production and design better fund
                                                                                                                                                                                                                                              Penttilae M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1714
                                                                                                                                                                                                                                                         Uusitalo J,
                                                                                                                                                                                                                                                                                   TUTKIMUSKESKUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                          Huuskonen
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                                                                                                                                                                          able protein,
fungal strai
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t directly from
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AAQ58017/c
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pMLO16del0(2) was used as a PCR template to yield a 280 bp fragment E (primers = AAQ58023 and AAQ58024), beginning at the promoter internal polylinker and ending at -720, and a 720 bp fragment F (primers = AAQ58026 and AAQ58028), beginning at -720 and ending at KspI at -16. Fragments D and E were purified from agarose gel and digested with BstEII-XbaI and XbaI-KspI respectively,& ligated to the 7.8 kb BstEII-XspI fragment of pMI-25 to produce produce
                                                                                                                                                           Ilmen
                                                                                                           Cloning promoters active in used partic for expression
                                                                              Example; Figure 18B; 120pp; English.
                                                                                                                                                                                                                                                                                                  Sgo
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14-SEP-1994
                                                                                                                                         WPI; 1994-083192/10
                                                                                                                                                                               (ALKO-) ALKO OY AB.
                                                                                                                                                                                                 19-AUG-1992;
                                                                                                                                                                                                                    19-AUG-1993;
                                                                                                                                                                                                                                        03-MAR-1994.
                                                                                                                                                                                                                                                          W09404673-A1
                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoter; cellobiohydrolase 1; cbh1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ58017 standard;
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                                                                                                  glucose-contg. medium
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                                                                                                                                                          Nakari TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     altered cellobiohydrolase 1 (cbhl) promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
                                                                                                                                                                                                                                                                                                                       /label= deletion site
9 1054..1059
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                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 704..709
                                                                                                                                                                                                                                                                              /label=
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/label= altered sequence
1774..1776
                                                                                                                                                                                                                                                                                                                                                           748..749
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/label= polylinker
                                                                                                                                                                                                                                                                                                                                                                                       16..748
                                                                                                                                                                                                                                                                                                                                                                                               *tag= a
label= altered sequence
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42.00
84.62%
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51.22%
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                                                                                                                                                            Nevalainen
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of genes i
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                                                                                                                                                          KMH,
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Indels:
Gaps:
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Matches:
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                                                                                                            d environmental in Trichoderma
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                                                                                                          condition -
fungal hosts
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                                                           bp fragment
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RESULT 38
AAQ58018/c
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity:
      WPI; 1994-083192/10
                                                                                                 03-MAR-1994.
                                                                                                                                                         SgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pMI-27. The cbh1 promoter of pMI-27 has sequence alterations at posns. -1505-1500 (genomic sequence GTGGGG, altered sequence TCTAAA) and at posn. -720 to -715 (genomic sequence GTGGGG, altered sequence TCTAGA) upstream of the translation initiation codon of ir cbh1 promoter. The sequence of the altred cbh1 promoter in pMI-27 is provided in AAQ58017.
                          Ilmen
                                                             19-AUG-1992;
                                                                               19-AUG-1993;
                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                    misc_feature
                                           (ALKO-) ALKO OY
                                                                                                                    WO9404673-A1
                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                              Promoter;
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14-SEP-1994
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                        Nakari
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773..778
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716..748
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1774..1776
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Matches:
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RESULT
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G (primers = AAQ58023 and AAQ58025), beginning at the promoter internal polylinker and ending at -720, and a 720 bp fragment H (primers = AAQ58026 and AAQ58028), beginning at -720 and ending at Kspl at -16. Fragments G and H were purified from agarose gel and digested with BatEII XbaI and XbaI-Kspl respectively, & ligated to the 7.8 kb BstEII XbaI fragment of pM1-25 to produce produce pM1-28. The cbh1 promoter of pM1-28 has sequence alterations at posns. -1505-1500 (genomic sequence GTGGGG, altered sequence TCTAAA), -1001-996 (genomic sequence CTGGGG, altered sequence TCTAAA), and at posn, -720 to -715 (genomic sequence GTGGGG, altered sequence CTGTGGA) upstream of the translation initiation codon of intact cbh1 promoter. The sequence of the altred cbh1 promoter in pMI-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pMLO16del0(2)
G (prime:
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  Disclosure;
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                                New DNA sequence located in a promoter of a for optimized protein production and design
                                                                                                                                                        13-FEB-2001;
                                                                                                                                                                                13-FEB-2002; 2002WO-FI00116
                                                                                                                                                                                                                                                                                                                                       25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                     ABQ79594
                         protein
                                                                       WPI; 2002-657583/70
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                                                                                                                                                                                                                                                     Trichoderma reesei
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pdated on 25-MAR-2003 to correct PN field.)
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                       production
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                                                                                           Saloheimo
Archer D,
Page
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nttilae M;
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Indels:
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RESULT 40
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Best Local Similarity:
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                    The invention relates to a DNA sequence located in a promoter of a secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cbhl gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secretable protein, where the DNA sequence mediates transcriptional down-regulation of secreted proteins under secretion stress. The DNA sequence, promoter or the fungal host is useful to optimize protein production. The methods are useful to or to modify fungal strains for other purposes and selectively regulate the expression of certain undesired or desired proteins in the host. The present sequence represents a T. reesei DNA fragment located upstream of the cbhl gene promoter.
                                                                                                                                                Disclosure;
                                                                                                                                                                                          New
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter;
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                                                                                                                                                Page 76; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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enttilae M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secretion stress; fungal; cbhl;
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Alignment Scores:

Pred. No.:

42.00

Matches:

Percent Similarity:

Best Local Similarity:

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Conservative:

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Query Match:

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US-10-081-935-2 (1-18) x ABQ79597 (1-1874)

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Search completed: November 13, 2003, 12:08:30 Job time: 842 secs

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Sequence 1918, Ap
Sequence 15656, A
Sequence 9220, Ap
Sequence 9057, Ap
Sequence 18, Appl
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                                                                                                                                                                                                                                                                                     Sequence 132, App
Sequence 2891, Ap
Sequence 16275, A
Sequence 19, Appl
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7, Appli
9931, Ap
8, Appli
16386, A
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Sequence 2, Application US/09103840A

Redent No. 629428

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFREENCE: 2486-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                         6421, Ap
16212, A
10081, A
    1, Appli
18, Appl
20, Appl
10, Appli
1, Appli
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3, Appli
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US-08-1466-047B-18
US-08-1466-047B-20
US-09-254-733-1
US-08-254-733-1
US-08-254-733-1
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US-09-252-991A-16212
US-09-252-991A-10081
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Matches:
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Mismatches:
Indels:
Gaps:
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57.32%
  Percent Similarity:
Best Local Similarity:
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US-09-103-840A-2
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  Command line parameters:
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-O=/cgn2_1/USPTO spool/USIO081935/runat 12112003_144407_3656/app query.fasta_1.199
-DB=18sued_ Patents NA -OFWT=fastap -SUFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
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-USER=USI0081935_GCGN_1 1 44 @runat 12112003_144407_3656 -NCPU=6 -ICPU=3
-NO MMAAP -LARGEQUERY -NEG SCORES=0 -WATT -DSFBLCCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 34, Appl
Sequence 951, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
                                                                                     November 13, 2003, 11:51:07; Search time 52 Seconds (without alignments) 152.786 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:•
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:•
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:•
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:•
            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
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US-09-058-489-34

US-09-058-489-34

US-09-134-001C-959

US-09-134-001C-959

US-08-1389-564B-21

US-08-466-047B-22

US-08-466-047B-22

US-08-466-047B-22

US-08-389-564B-18
                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext 7
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                                                                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
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Match Length DB
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82
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4411529
1304
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Maximum DB seq
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                                                                 procein
                                                                                                                                                                      Sequence:
                                                                                                                                            Title:
Perfect :
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                                                                                        Run on:
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No.
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US-08-525-697-3
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No
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APPLICANT: Andersen, Lene N
APPLICANT: Andersen, Lene N
APPLICANT: Andersen, Lene N
APPLICANT: Andersen, Lene N
APPLICANT: Heldt-Hansen, Hans Hansen, Hansen, Hans Hansen, Hans
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                        1218600 TTCGCGCACGCCCTGGTGCGTCGTTGCCGCTGAATTGGCG 1218641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1219072 TTGGGGCGCGGCGTGTGGATGGCGCTGAATTGGCG 1219113
3 PheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAla 16
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4004.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/525,697
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                     Sequence 1, Application US/09103840A
Patent No. 629428
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08525697
Patent No. 5795764
GENERAL INFORMATION:
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47.00
92.86%
64.29%
57.32%
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TTORNEY/AGENT INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 4411529
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ADDRESSEE: No. 57957640 No. 5795764disk of No. 5795764th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ATGAAGCTTTCTCACATGCTCCTCAGCCTCGCCAGCCTGGGGGTGGCGACGCCT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READBLE FORM:
COMPUTER: ISBN DC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,697
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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TELECORDOR.: 212-86/----
TELEPHONE: 212-86/----
TELEPHONE: 212-86/----
TELEPHONE: 212-86/----
APPLICATION DMATA:
APPLICATION NUMBER: DK 0486/93
FTLING DATE: 30-APR-1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEFAN: 212-867-0123
TELEFAX: 212-878-9655
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0486/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Harrington, James J. REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DK 0
FILING DATE: 30-APR-1993
                                                                                                                                                                                                                                                                                                             3.04
44.00
77.78
44.44%
53.66%
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STATE: New York
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nuclei
STRANDEDNESS:
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/translation="MOFSHALIALVAAGLASAQLPDIPPCALNCFVEALGNDGCTRLT
DFKCHCSKPELPGQTTPCVEEACPLDARISYSNIVVDOCSKAGVPIDIPPVDTTAAPE
PSETAEPTEEPTEEPTAEPTAEPTAEPTHEPTEEPTAVPTGTGGGVPTGTGSFTVTGR
PTASTPAEFPGGGGVPTGTAALLGLAAYL"
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/t anslation="MRNSTMLNEPSISTTHIPSEGGPLGYPVSREDMKRGGTEWIEGT
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RQHLVFLLGGHGQRVQLDRPSAGEAEARGLLPRFHLKPRTDTNHIPPLCEPTPGGFYE
ARTSDLPHTWTTHTWTTHEOHTQPHSPYQDMRPDSETEEDSDTDGSHAYMELIED
DEDVLLDPDTFYDEFTEEHETNNTRERRLATSGQGDGLWGTPLHRHETHSNDHERLR
GWRWARRGERGAMMPAETFTCPQGRRPW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRL 29-JAN-2003
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Direct Submission
Submitted (05-FBB-2002) MRC Virology Unit, Church Street, Glasgow G11 5JR, U.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimpanzee cytomegalovirus
Uiruses, tompanzee cytomegalovirus
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.

1 (bases 1 to 241087)

2 obvison, A.J., Dolan, A., Akter, P., Addison, C., Dargan, D.J.,
Alcendor, D.J., McGeech, D.J. and Hayward, G.S.
The human cytomegalovirus genome revisited: comparison with the dimpanzee cytomegalovirus genome
J. Gen. Virol. 84 (Pt 1), 17-28 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear

    .241087
    /organism="Chimpanzee cytomegalovirus"

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18
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimpanzee cytomegalovirus, complete genome.
AF480884
                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:188763"
1. .687
/rpt_family="TRL"
/rpt_type=inverted
1. .297
/note="terminal redundancy"
                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241087 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714. .1628
/codon_start=1
/product="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="a"
688. .200038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF480884.1 GI:19881028
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100.00$
100.00$
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                           BASE COUNT
                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF480884/c
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                        Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                       ORIGIN
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                                         /organism="Coccidioides posadasii"
/proganism="Coccidioides posadasii"
/mol type="genomic DNA"
/strain="Silveira"
/db xref="taxon:199306"
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/product="antigen 2"
/product="antigen 2"
/product="antigen 2"
/protein id="AAC49612.1"
/db xref="GI:1256444"
/db xref="GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF011256 3821 bp DNA linear PLN 22-AUG-2000
Coccidioides immitis proline rich antigen (PRA) gene, complete cds.
AF013256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. (bases 1 to 3821)
Peng,T., Orsborn,K.I., Orbach,M.J. and Galgiani,J.N.
Direct Submission
Submitted (09-JUL-1997) Infectious Disease, University of Arizona, 1501 N. Campbell, Tucson, AZ 85724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 382)
Peng,T., Orsborn,K.I., Orbach,M.J. and Galgiani,J.N.
Proline-rich vaccine candidate antigen of Coccidioides immitis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .3821
/organism="Coccidioides posadasii"
/mol_type="genomic DNA"
/strain="Silveira"
/db_xref="taxon:199306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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/gene="PRA"
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/gene="PRA"
/note="antigen 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/protein_id="AAB66894.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spherule maturation
J. Infect. Dis. 179 (2), 518-521 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-081-935-2 (1-18) x CIU51200 (1-1435)
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF013256.1 GI:2331288
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100.00$
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join(737. .9
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Best Local Similarity:
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                            source
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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SVEEEQYRRVVGNYTRRRHHPQHRSYRRRNALVANGRDSLLLARLRINHQRQYRFTGY
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RQASRRIRTRWEEENTVMSDAASRLRAWFSRRTTYWQRTWVPGENPSAEAGELAVPPA
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                                                                                                                                                                                                                                                                                                                               'note="RL11 family"
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SYNEPRADDDWGTYEDPFLAYRDLTRKKLDSHASKKQNIYERIPYRPCRQLRDDEPP

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|/translation="MRGDAVSILIVEDLDLPSFGSFNASHAYYSFRVLRGIFYVTVVV
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LKPAGTNPPPNDLRDWMLNISIHCAWIAGLLIVASLVGFLLRLRRVGVQNAYRRLSN
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TIFNPTEDGWGIYSLVTESPFLNDNKHYTAEFYVTIDTRNNGTBEELDYDYDDYGSGF
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                                                                                                                                                                                                                                                               'note="RL11 family"
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinera strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerae during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOLTYLIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
                                                                                                                                                                              Eukaryota; Fungi; Ascomycota, Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1. Levis, C. Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 660)
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AL11334.1 GI:582853
CDNA library, nitrogen deprivation.
CDNA library, nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
Bitton,F., Levis(0)
Bitton,F., Levis(0)
Direct Submission
                                         CNSO1AO7

CNSO1AO7

CNSO1AO7

CNSO1AO7

CONGINE CINERA STRAIN T4 CDNA library under conditions of
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215 c 132 g 153 t
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/mol type="mRNA"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                           CDNA library; nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-081-935-2 (1-18) x CNS01AO7 (1-660)
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                                                                                                            AL113183.1 GI:5827802
                                                                              nitrogen deprivation.
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72.22%
55.56%
58.54%
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Direct Submission
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Best Local Similarity:
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                                       LOCUS
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EEFTKGGADATTTVTASETTDDVIQTNELPCELNNAEEISSGRAVVGTCPRREGPHR
SFRELCLGIWASSHLARRAISVS"
18719...19780
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.

The library was produced in an oriented direction, in the pBSII
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AL112861.1 GI:5827480
CDNA library; nitrogen deprivation.
EDUTYORINIA fuckeliana
Botryotinia fuckeliana
Botryotinia fuckeliana
Botryotinia, Solerotiniaceae; Botryotinia, Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 660)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
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Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
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/strain="T4"
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PLN 03-SEP-1999

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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage: CP 5706 91057 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerae strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerae during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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2 (bases 1 to 696)
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Botryotinia fuckeliana
Botryotinia fuckeliana
Botryotinia fuckeliana
Bukaryotea; Fungi, Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.

1 (Basea I to 656)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

Direct Submission
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Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
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/noTe="Genoscope sequence ID : W32D051"
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//mol_type="mRNA"
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr The be. : www.genoscope.cns.fr) The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal asituation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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CDNA library, nitrogen deprivation.
CDNA library, nitrogen deprivation.
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/organism="Botryotinia fuckeliana"
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Score

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697 10 3 5 0

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Direct Submission
Submitted (01-SEP-199) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
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    The library was produced in an oriented direction, in the pBSII
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1 (Dases 1 to 720)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

Direct Submission

Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Botryotinia fuckeliana"
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/mol_type="mRNA"
/strāin="T4"
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/db_xref="taxon:40559"
/note="Genoscope sequence II
a 219 c 151 g 149 t
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cDNA library, nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
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221 c 145 g 174
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                                                                                                                                                                                                                                             Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr | The cDNA library to be analyzed within the framework of this project was created using a Botrycis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal alitution for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
                                                    Eukaryota; Fungi; Ascomycota, Pezizomycotina, Leotiomycetes, Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 696)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
Direct Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
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CDNA library; nitrogen deprivation.
Botryctnia fuckeliana
Botryctinia fuckeliana
Botryctinia fuckeliana
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryctinia.
1 (bases 1 to 697)
Bitcon, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
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/mol_type="mRNA"
/strain="T4"

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/note="Genoscope sequence ID
212 c 148 g 161 t
cDNA library, nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
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RESULT 14 AC010228

ACCESSION VERSION KEYWORDS

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Consensus quality: 146731 bases at least Q40
Consensus quality: 146937 bases at least Q30
Consensus quality: 146937 bases at least Q30
Consensus quality: 147107 bases at least Q30
Estimated insert size: 0; mull estimation
Estimated insert size: 147808; sum-of-contigs estimation
Quality coverage: 2.147836E7; in Q20 bases; null estimation
Quality coverage: 30.25 in Q20 bases; null estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                           ACLISU471

148008 bp DNA linear HTG 10-AUG-2002
Homo sapiens chromosome 5 clone RP11-420M3, WORKING DRAFT SEQUENCE,
Junordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                             AC13047.1 GI:22203244
HTG: HTGS PHASEL; HTGS_BRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
5755 CTCCAATTTACAAGGATATTACTGACTTTAGTATCTGCAGGAATGGCCAGT 5805
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11 2353: contig of 1253 bp in length
12 4513: gap of unknown length
14 18008: contig of 14555 bp in length.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
Center Project Name: 567936
Center clone name: RPCI-11_420M3
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/clone="RP11-420M3"
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2 (bases 1 to 148008)
DOE Joint Genome Institute.
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Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 17 (Dases 1 to 78680)

DoE Joint Genome Institute.

Direct Submission

L. Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute and Stanford Human Genome Center.

Direct Submission

L. Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (Dases 1 to 78680)

S. Dose Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

L. Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (Dases 1 to 78680)

S. Dose Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 60 Juli 16, 2002 this sequence version replaced gi:21637453.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                        PRI 16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford Human Genome Center
Finishing Completed stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 145.4kb). It is clipped at the overlap with AC008955.
The number of bases overlapped is 9996.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                             Homo sapiens chromosome 5 clone CTC-298B17, complete sequence. AC010228 B GI:21844555 HTG.
                                                                              1 (bases 1 to 78680)
DOE Joint Genome Institute and Stanford Human Genome Center
                                                   1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
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/organism="Homo sapiens"
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US-10-081-935-2 (1-18) x CNS01AOB (1-720)
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AUTHORS TITLE JOURNAL

REFERENCE

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AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

BASE COUNT ORIGIN

FEATURES

Pred. No.:

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 16

AC011421

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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COMMENT

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SE (Dases I to 175178)

S Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R. Boguslavkiy, L., Boukhgalter, B., Baddwin, J., Barna, N., Deckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Horton, L., Howland, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McEwan, P., McGurk, A., Morman, C.H., O'Connor, T., O'Donnell, P., McEwan, P., Norman, C.H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Talamas, J., Talamas, J., Talamar, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Buretted (14-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 3, 2000 this sequence version replaced gi:6446867.

All repeats were identified using RepeatMasker: html
http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                     Homo sapiens clone RP11-16L10, LOW-PASS SEQUENCE SAMPLING.
AC011783 GI:7144945
HTG; HTGS DHARCA
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175178)
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                         1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seg.wi.mit.edu
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TITLE
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JOURNAL
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Homo sapiens chromosome 5 clone CTD-230305, complete sequence.
AC011421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 148142)
DOE Joint Genome Center and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (23-OCT-1999) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 148142)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Dioc Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell

Brive, Walnut Creek, CA 94598, USA

On Oct 23, 1999 this sequence version replaced gi:6013521.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 148142) DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (02-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 148142)
DOE Joint Genome Institute and Stanford Human Genome Center.
                  www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
STS Content:
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26865 c 24848 g 45853
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DOE Joint Genome Institute.
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                                                                                                                                                                                                    tuberculosis complex.

1 (bases 1 to 1448)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Mivula, A. and Bishai, W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
                                                                                         Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished

[ (bases 1 to 14483)

[ (bases 1 to 14483)

[ Eleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Khouri, H., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA
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complement(66. .560)
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complement(746. 1207)
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/gene="MT1111"
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| 1282. 2116
  AE006992 AE000516
AE006992.1 GI:13880691
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/transl_table=
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section 78 of 280 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 377)
Feldmann, A.
Direct Submission
Submitted (08-JAN-2000) Feldmann A., Institut fuer Virologie,
Philipps Universitaet Marburg, Robert-Koch-Str. 17, 35037 Marburg,
GERMANY
                                                                                                                                                                                  Gallus gallus partial mRNA for proprotein convertase PACE4 (PACE4 AJ252171
                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feldmann, A., Schafer, M.K., Garten, W. and Klenk, H.D. Targeted infection of endothalial cells by avian influenza virus A/FPV/Rostock/34 (H7N1) in chicken embryos
J. Virol. 74 (17), 8018-8027 (2000)
                                1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
                                                                                                                                                                      linear
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                      mRNA
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PACE4 gene; proprotein convertase PACE4
Gallus gallus (chicken)
Gallus gallus
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Mycobacterium tuberculosis CDC1551,
complete genome.
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                                                                                                        RESULT 18
GGA252171/c
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/codon_start=1
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9692. .9859
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RFPDAGEPWTVSKLYYVHGFLRERMQMLQDEFARHGQRGPFEGWLAYWDPDHDFLTSR
VTTRVECSKYFSQRDDALRAHATQIDPNAEFFAAPLAWQERLWPTEFFLARSRIPAR
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2398. .4419
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                                                                                                                              2145. .2411
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/gene="MT1116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3357. .6145
/gene="MT1118"
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                                                                       PPETELFAGIEP"
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CDS

CDS

CDS

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PUBMED
REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                          RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 26, 1998 this sequence version replaced gi:2896684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.

Beciphering the secondary of Mycobacterium tuberculosis from the complete secondary of Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence Nature 393 (6685), 537-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis H37Rv Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 67200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
/note="Rv1049, (MTV017.02), len: 148. Probable repressor similar to many e.g. P74870 (149 aa). FASTA scores: sptr|P74870|P74870NEGATIVE REGULATOR OF EME LOCUS EMR (149 aa) opt:146 z-score: 200.3 E(): 0.0011; 31.6% identity in 95 aaoverlap. TBparse score is 0.892. Contains probable helix-turn-helix motif at aa 58-79 (Score 1495, +4.28 SD)"
                                                                                                                                                                                                                                              /gene="Rv1049"
184. .630
                                                                                                                                                                                                                                                                                                                                                                                                  /note="fragment
physical clone"
                                                                                                                                                                                                         /gene="Rv1049"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mycobacterium"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="taxon:83332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .66170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                      possible
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                                                                                                                                                                                                                                                                                                                                                                                                                             designated v017.
                                                                                                                                                                                                                                                                                                                                  ggag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis H37Rv"
                                                                                                                                                                                                                                                                                                                                  for Rv1049
                                                                                                                                                                                                                                                                                                                                                                                                                      Does not represent a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBS
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3521 .3910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to protein encoded by Lactococcus lactis plasmid pNP40, LLU36837 2 (298 aa). FASTA scores: U36837|LLU36837-2 Lactococcus lactisplasmid pNP40, (298 aa) opt: 194 z-score: 245.5E(): 3.5e-06; 30.3% identity in 155 aa overlap. TBparse score is 0.912. Contains possible helix-turn-helix motif at aa197-218 (Score 1097, +2.92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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/krvanelation="MARQRFRDQVVLITGASSGIGEATAKAFAREGAVVALAARREGA
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AMHAIAGFSDALRQELRGSGIAVSVIHPALTQTPLLANVDPADMPPPFRSLTPIPVHW
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PGLRVRVAMSVGPWQGIAAWDVSTGEPIAPWPTRVTIDRILGEPITLLGYAPETIIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SD) "
                                                              /translation="MDCCEERGVARHKGLSQVGTPGCPRWSQAVSCRCSAYREAAVTA
VQMPLTPGYGETPLPHDELAALLPEVVEVLDKPITRADVYDLEQGLQDQVFDLLMPTA
VEGSLSLDELLSDHFVRDLHARMFGPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv1050, (MTV017.03), len: 301. Probable oxidoreductase similar to many e.g. MTCY48.22C(341 aa). FASTA scores:sp[010783|Y04M_MYCTU PUTATIVE OXIDOREDUCTASE CY48.22C (341aa) opt:462 z-score: 533.9 E(): 3e-22; 33.6% identity in265 aa overlap. TBparse score is 0.896"
'gene="Rv1053c"
                                  complement (3809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIGPASFTLGRRVVYRRDEVSRWISKRESATRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGVTILERGITSTRWRDYVDIVQLDRRGIDDDELLRSARAVAQYRGATLEPVAPHLAG
YGAVAQAKWATEHGRCQHCWRHWKPAHVGRRNMDLLDAKQVSEMIGVPVGTLRHWRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1743. . 2498)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv1050"
679. .1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="possible 679. .1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MGKGAAFDECACYTTRRAARQLGQAYDRALRPSGLTNTQFSTLAVISLSEGSAGIDLTMSELAARIGVERTTLTRNLEVMRRDGLVRVMAGADARCKRIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="possible RBS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rv1051c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein Rv1049"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKGRAALQKAVPLWRGVQAEVTASVGDWPRVRRDIANLGQAAEACR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Rv1050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:053397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                          (MTV017.05), len: 129. Unknown"
                                  .4084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaggtgg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for Rv1052"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                             RESULT 21
AC144792
                                             VERSION
                                                                         ACCESSION
                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                     US-10-081-935-2 (1-18) x MTV017 (1-67200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                          KEYWORDS
                                                                                                                                          POCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sg
                                                                                                                                                                                                                               46872
                                                                                                                                                                                                                          AC144792 210652 bp DNA linear HTG 20-MF Mus musculus chromosome UNK clone RP24-501M24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
AC144792 AC144792.1 GI:30911145
HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Rv1055"
4935. .5171
/gene="Rv1055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv1054" (MTV017.07), len: 68. Unknown but similar /notes"Rv1054, (MTV017.07), len: 68. Unknown but similar to hypothetical Mycobacterium tuberculosis protein MTCY3G12_25 (151 as shows similarity to integrases) and to Mycobacterium paratuberculosis integrase MSGINT 1 (191 as). This orfcontinuesin another frame as MTV017.08 but no error can befound toaccount for frameshift. FASTA scores: 79702 MTCY3G12_25 (151 as) opt: 273 z-score: 364.1 E(): 8.8e-13; 64.7% Identity in 68 as overlap; and L39071 MSGINT 1 (191as) opt: 105 z-score: 148.5 E(): 0.9; 31.8% identity in 85 asoverlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Rv1055, (MTV017.08), len: 78. Partial orf, first /19aa similar to hypothetical Mycobacterium tuberculosis protein MTCY3G12_25 (151 aa shows similarity to integrases) andto Mycobacterium paratuberculosis integrase L39071|MSGINT_1 (191 aa) and to many other integrases or transposases. FASTAscores: Z79702|MTCY3G12_25 (151 aa) opt: 291 z-score:428.6 E(): 2.2=16; 74.3% identity in 70 aa overlap; anddp|L39071|MSGINT_1 (191 aa) opt: 146 z-score: 291.0 E(): 8.3e-05; 52.1% identity in 48 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Rv1054"
4726. .>4932
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/transl_table=
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/protein_id="CAA17170.1"
/db_xref="GI:2896691"
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein Rv1053c'
/protein_id="CAA17169.1"
/db_xref="GI:2896690"
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/transl_table=
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/note="Rv1053c, (MTV017.06c), len: 91. Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein Rv1055"
/protein_id="CAA17171.1"
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US-10-081-935-2 (1-18)

x AC144792 (1-210652)

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                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
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12436
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/note="assembly name:Contig20"
<sub>4 48568 c 48742 g 58398 t</sub>
                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig18"
37934. .94620
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                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig17"
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                                                                                                                                                                                                                                                    /note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                             12436. .37833
                                                                                                                                                                                                                                                                                                                                                                                           clone="RP24-501M24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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12435: gap of unknown length
37833: contig of 25398 bp in length
37933: gap of unknown length
94620: contig of 56687 bp in length
94720: gap of unknown length
94720: gap of unknown length
210652: contig of 115932 bp in length
                    47.00
82.35%
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex 15, France. e-mail:tgarnier@pasteur.fr Submitted on behalf of the Mycobacterium bovis sequencing teams. TB Research Group, Veterinary Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone, Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK. P74 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nycobacterium bovis subsp. bovis AF2122/97
Hacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of Mycobacterium bovis online Publication PNAS 10.1073/pnas.1130426100 ( Microbiology ) 2 (bases 1 to 327650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S., Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L., Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garnier,
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327650 bp DNA linear BCT 11-JUN-2003
Mycobacterium bovis subsp. bovis AF2122/97 complete genome; segment
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Mycobacterium bovis subsp. bovis AF2122/97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="Mb0912"
/note="Mb0912, -, len: 490 aa. Equivalent to Rv0888, len: 490 aa, from Mycobacterium tuberculosis strain H37Rv, 490 aa, overlap). Probable exported protein. Equivalent to AAK45157.1 from Mycobacterium tuberculosis strain CDC1551 (507 aa) but shorter 17 aa.
                                                                                                               KKSKMPSQTPPEPPTLLWPIGVPFSDGLNTLSEFKVQRLDRQTWYECTSDNCLTLKGF
TYSQMRLPGGDTVDVYNLHTNTGGGPTTNANLAQVANYIQQNSAGRAVIVTGDFNARY
SDDQSALLQFAQVNGLTDAWVQVEHGPTTPPFAPTCMVGNECELLDKIFYRSGQGVTL
                                                                                                                                                                                                        ENRTPVANPOQVSVPEGGTVGPVRFDACDPDGNRMTFAVRERGAPGGPQHGIVTVDQR
TASFIYTADPGFVGTDTFSVAVVSDDTSLHVHGLAGYLGPFHGHDDVATVTVFVGNTPT
DTISGFSMLTVNIAGLPFPLSSAILPRFFYTKEIGKRLNAYYVANVQEDFAYHQFLI
                                                                                            QAVSYGNEAPKFFNSKGEPLSDHSPAVVGFHYVADNVAVR"
                                                                                                                                                                                                                                                                                                 translation="MDYAKRIGOVGALAVVLGVGAAVTTHAIGSAAPTDPSSSSTDSP/
VDACSPLGGSASSLAAIPGASVPQVGVRQVDPGSIPDDLLNALIDFLAAVRNGLVPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains possible N-terminal signal sequence
/gene="citA"
/locus_tag="Mb0913c"
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/db_xref="GI:31617664"
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/strain="AF2122/97"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .327650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tag="Mb0912"
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/locus_tag="Mb0914c"
complement(3413..6061)
/locus_tag="Mb0914c"
/locus_tag="Mb0914c", len: 882 aa. Equivalent to Rv0890c,
/locus_mb0914c, len: 882 aa. Equivalent to Rv0890c,
/note="Mb0914c, len: 882 aa. verlap). Probable
transcriptional regulatory protein, LuxR family, highly
similar (but shorter 238 aa in N-terminus) to
NP 302202.1|NC 002677 possible transcriptional regulator
from Mycobacterium leprae (1106 aa). Also highly similar
(generally in part) to others e.g. T50568 probable
multi-domain regulatory protein from Scentring coelicolor (134 aa); P10957|NARL ECOLI nitrate/nitrite
response regulator protein from Escherichia cooli (216 aa),
FASTA scores: opt: 193 E(): 6e-06, (37.4% identity in 99
aa overlap); etc. Also highly similar co others from
Mycobacterium tuberculosis e.g. MTCV02B10 22, MTV008 44,
MTV036_21, and MTCY31_24. Contains PS00017 ATP/GTP-bInding
site motif A (P-loop), P300622 Bacterial regulatory
proteins. luxR family v signature. and probable helix-turn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/product="PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN
/probably LUXR-FAMILY)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ien: 373 aa, from Mycobacterium tuberculosis strain H37RV, (100.0% identity in 373 aa overlap). Probable citA (alternate gene name: glth), citrate synthase 2 (EC 4.1.3.7), highly similar to others e.g. CAB95899.1|AL359988 putative citrate synthase from Streptomyces coelicolor (387 aa); P39119|CISY BACSU citrate synthase II from Bacillus subbilis (366 aa), FASTA scores: opt: 586, E(): 5.0e-30, (33.0% identity in 367 aa overlap); etc. Also similar to Rv0896|MT031.24 from Mycobacterium tuberculosis (29.3% identity in 274 aa overlap) and Rv1131. Contains P500480 Citrate synthase
                                         DVPTKVLGLYTQAQVLAYCGASAAHAIAGACIAAATELGGVYQGIGYAAMTYAALAAG
DVTAALEASDAARPILRAQPDQVTMHQVLMAQLALAGGDAIAARQFANDAVDATNGWH
RMVALTIRARVATARGEPELARDDAHAALACGAELHIYQGMPDAMELLAGLAGEVGSH
                                                                                                                                                                  DHORLVARAETEIDNIRAAFAWSRENGHITEALOLASSLOPIWEGRAHLREGLSWENS
ILBOORFHRLAVSTAVRARALAADKANLSTHAATSVGATDIIABAQQALAMAREVGODP
AALVRALTACGCSSGYNAEAAAAPYFAEATDLARAIDDKWTLCQILYWRCVGTCISGSD
NALRAAAEECRDLADTIGDREVSRHCSLWLSLAQMWAGNLTEALELSREITAEAEASN
                                                                                                                                                                                                                                                                                                                                                  ELLGACPELTI LATSREPI GMAGEI TWRVPSMS I TDEAVELFADRASRVQPGFTI ANH
NAAAVGEI CRRLDGI PLAI EFAAARVRSMS PLEI ADGLDDCFRLLAGGVRGAVQRQQT
LRASI DWSHALTETEVGLI EFRRLAPFVGGFDLAAVRAVAAGSDLDFFSVLDQLTILVD
KSLVVADDCQGRTRYRLLETVRRYALEKLGDSGEADVHARHRDYYTALAASLNTPADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, luxR family signature, and probable helix-turn helix motif from aa 836 to 857 (Score 1559, +4.50 SD). BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL REGULATORS."
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VAVAVEQAALSELRERRPDRAIETNVEFWAAVVLDFARVPANMMPAMFTCGRTAGWCA
HILEGKRLGKLVRPSAIYVGGGPRSPESVDGWERVLTTA"
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Qrvftgdwallvogenfgsgldpaepepplp iisgdvrvdvqaglamlapimgyaplld
Iddatarqolarasywalsyvaqsarggiydpavpqriidegstyvtarpmtrwqoepbp
RHIEAIDAYWVSAAEHGMNASTFTARVIASTGADVAAALSGAIGAMSGPLHGGAPARV
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/codon_start=1
/trans1_table=11
SEGVRLLGAAAALRQQTRQVRFKIWDAGYQASVTALREAMGDEDFDRAWAEGAALSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATORS.
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/protein_id="CAD93774.1"
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CDS

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Query Match:
DB:
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US-10-081-935-2 (1-18) x BX248337 (1-327650)
                                                                                                                              Best Local Similarity:
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/EC_number="1.14..."
/note="Mb0916, -, len: 495 aa. Equivalent to Rv0892, len: 495 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 495 aa overlap). Probable monooxygenase (EC 1.14.-.), highly similar to others e.g. NP_250787.1 NC 002516 probable flavin-binding monooxygenase from Pseudomonas aeruginosa (491 aa); CAB59668.1 AL132674 monooxygenase from Streptomyces coelicolor (519 aa); P12015 CYMO ACIS Cyclohexanone monooxygenase from Acinetobacter Sp. (542 aa), FASTA scores: opt: 489, E(): 6.8e-26, (30.3% identity in 492 aa overlap); etc. Also highly similar to Rv0565c, Rv3854c, Rv3083, etc from Mycobacterium tuberculosis. Has
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                                                                                                                                                                                                                                                                                                                                        /translation="MTGRCPTVAVVGAGMSGMCVAITLLSAGITDVCIYEKADDVGGT WRDNTYPGLTCOVPSRLYQYSFAKNPNWTQMFSRGGEIQDYLRGIAERYGLRHRIRFG ATVVSARFDDGRWVLRTDSGTESTVDFLISATGVLHHPRIPFIALGLDDFRGTVFHSAR WDHTVPLLGRRIAVIGTGSTGVQLVCGLAGVAGKVTMFQRTAQWVLPWPNPRYSKLAR VFHRAFPCLGSLAYKAYSLSFETFAVALSNPGLHRKLJVGAVCRASLRRVRDPRLRRAL TPDYEPMCKRLVMSGGFYRAIQRDDVELVTAGIDHVEHRGIVTDDGVLHEVDVIVLAT GFFDSHAFFRPMCLTGROIR IDVWQDGPHAHQTVALFGFPNFFMMLGPHSPYGNFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLFNAVHNSLPPNIDIDHAILRGEDHPPTCAKCVARGRISALGS
LDLRYKIRCYAAPPDVGRCEEVPPRRRVLIANGGLDVGRLPPGTVTLLLADVEEST
HLWQMCPEDMATAIAHLDHTVSEAITNHGGVQPVKRYEGDSFVAAFTRASDAAACALD
LQRTSLAPIRLRIGLHTGEVQLRDELYVGPTINKTARLRDLAHGGQVVLSAATGDLVT
GRTPADAMLVDLGRHPLRGLPRPEWVMQLCHPDIREKFPPLRTAKSSPTSILPAQFTT
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THVYAKLGLASRVQLVDEAARRGSPS"
                                                                                                                                                                                                                                                                                                                       TAVAESQAEHI VQWI KRWRHGEFDTMEPKSAATEAYNTVLRAAMPNTVWTTGCDSWYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrophobic stretch at N-terminus."
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7318. .8805
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/protein_id="CAD93776.1"
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/note="Mb0915c, -, len: 285 aa. Equivalent to Rv0891c,
len: 285 aa, from Mycobacterium tuberculosis strain H37Rv,
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/db_xref="GI:31617668"
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/transl_table=11
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                                                                                     Matches:
Conservative:
Mismatches:
Indels:
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PheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAla

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AUTHORS
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SOURCE
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DB:
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MEDLINE
PUBMED
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G32057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Animal Breeding
Wageningen Agricultural University
Box 318, 6700 AH Wageningen, The Netherlands
Email: richard.crooijmansgealg.vf.wau.nl
Primer A: GGAGAGAGACAACTGTATTC
Primer B: AGGGTGAGAGAGTACAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1204)
Crooijmans,R.P., Dijkhof,R.J., van der
New microsatellite markers in chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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Gallus gallus
                                                                                                                                                                                                                                                        size
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Total Vol:
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/db_xref="taxon:9031"
/clone_lib="Chicken R
                                                                                                                                                                                                                                                                                                                                                                                                        dNTPs:
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46.00
92.31%
69.23%
56.10%
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jmans Gallus gallus STS genomic, sequence
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                                    Length:
Matches:
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chicken optimized
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C for 30 seconds
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RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haas, J., Woessner, J.P. and Waffenschmidt, S.
Direct Submission
Submitted (18-MAY-2001) Institute of Biochemistry, University
Cologne, 47 Zuelpicher Str., Koeln 50674, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waffenschmidt, S., Woessner, J.P., Beer, K. and Goodenough, U.W. Isodityrosine cross-linking mediates insolubilization of cell walls
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Chlamydomonas reinhardtii hydroxyproline rich glycoprotein Vsp6
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GOVNNIRANFESGASALVHETMHHLGMAHFAVGECVDDDASTGVTDTPESSGPVMSQP
WAQKAYIGCMAMMUKVLTSUMMDTAMRQASLRVGIPTTDVUPAFDSCBSGSDETANY
ITYTVDICQLAMGHLTSGQITAMHQITADNNPTLYAMGQYYAQNPPAGYTPPVAATPS
PSRKBSPSPSPKSPSPSPSPSPSPSPCTNAFGESBCKMCQVDRSNGCOMANARUGMTBYTDYTGCGSTNNCACKCVNSWSYQNNQYS
DCVTAPGEEDSKGNMCQVDRSNGDCANARUGMTBYTDYTGCGSTNNCACKCVNSWSYQNNQYS
PTNSGGTPNCGAGATTKQGLTCTMNNMKLKDSTTVYQGCANPNNAPKGSMCVLAKGSP
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IIRAFMPIDYERNANNKAIQTHYDQTTSILNPAFHALSADISSVGGTNATYDPNVLRIY
VLSKYKGGSQDLLARLERWAHGLOVSDDFNAQLYQLTTSLADVFGYIRDNGSKWGTTASG
PGGRRULAANSAERWLQLVKAFIKSGLOAPALQGRLGDLTPMFGDVDAIVDLVVDLWN
SIRGIAANSAERWLQLVKAFIKSGLOAPALQGRLGDLTPMFGDVDAIVDLVVDLWN
SIRGIAABANSIAASQQDYHPS FEPPPFPUQYGNNVNSULTWNII IAGEEGDDIVQ
DVPRGSSRRULDQNQIV VIPLPAGFTPQKFANLFTVLIPLVWHIMMYQNGGTYYGPBG
VDKACSSRRRULDQNQIV VIPLPAGFTPQKFANLFTVLIPLVWHIMMYQNGTGTYGFGY
YDKACDMAHGMIAIANFRLMFARFQLFLQECRNTPSYQYLIKPSRDRWINCASPGFFY
                                                                                                                                                                       PLRFGWDYCPDACNTAAPPADTASYPQGIHCKNGFTGLPGTSCTCSNSYAISFQGIGT
KYTGQSGCTEFEETGSGMCVTTCTKNADKSFNNKPYTCACK"
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|protein_id="AAK60544.1"
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/note="cell wall
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|mol_type="mRNA"
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Chlamydomonas reinhardtii hydroxyproline-rich
mRNA, complete cds.
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TGERTYGRSEYTWDLPWRLLTVIGIVILLAGEGGGGAGAWGARGVNONEEPCTIQVSG
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NATIDPNVLRIYVLGKYEGDQDVVASSSTSRTLQISPDFFENILEITTGLVDIFNYIR
DNNSKIGTTSAASGRRALLQSSSSNQPLPSQVLAAFIKSGLQSFTLQGALGDLTFIFS
DIDNISKIGTTSAASGRRALLQSSSSNQPLPSQVLAAFIKSGLQSFTLQGALGDLTFIFS
DIDNIASLAVDTYFAIKDLAHBVDSMGVVMNNYHPESPTAPPSVTEPLTIGGFTNSSV
QVTVSYDLLVVGBATEDAVATVPSNGRRLLQDNQIVIFLPLAGFTPGKPADLPNVLIFL
VFHVMLYSNGDGTYGPPGIANSLAMAHGMVAIANYRLQPAKIQLFVQEVRASPSFQYS
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TDDPFYGHMGLTWTTFSTDGVNNRASYESGASALVHETMHLGMMHTFSDGTCGDDDA
PSVSDTPSTNGFVMSQDWAQKAYIACMAMSKSLSAMWDTANRQASLRVGIPANDANS
AFDSCPSSAGADETANYITYTYDICLLVLGHLTSGQVVAMHQITADNNTTLYAMGQYY
ANNEACHORD
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                                                                                                                             CANARNGWWDYCTPSCGTNPAPSPSPSPSPSPSPSPTSTGGTPSCGAGAPTKSGLTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hydroxyproline-rich glycoprotein VSP4"
/protein_id="AAK83527.1"
/db_xref="GI:15145803"
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/mol_type="mRNA"
/db_xref="taxon:3055"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thesis (2001) Department of Pathology, University of Cambridge, Cambridge, United Kingdom 2 (bases 1 to 8117)
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LLAKLAWNFSPEGLDHLFDCFKASWTNASKKQREKLLELIRLBEDDXDGVWAHKVLM
LLWLLAWNFSPEGLDHLFDCFKASWTNASKKQREKLLELIRLBEDDXDGVWAHKVLM
LLWLAHSDDVEVDIMOLALSAHIKILDYSGSQDRDTQKIQHIDCFILEFRTINKMVI
PALKQIKEICSLFGEAFQNLSQCHQSFRVFYRHDLISQLQHHHALVTLVABNLASYM
SIRLYARDHEDVDPQTWRLGSRYSHVQEVQEBLNFLRFLLKDGQLHLCVSQAKQIWNC
LAENAVFSDREACFMWYSKLMGDEPDLHPDINKEFFESNVLQLDFSLLTENGMKCFE
RFFKTWLGREGKLMIKRKIYMMDDLDLIGLDYLWKVVIQSNDDISSRAIDLJKEIYTS
LGPKLQANQVVIHEDRILGSCFDRLKASYDTLCVLDSEKDNIFSCARQEAIRMWRILTV
LREYISEYDDSDYHEERMILPMSRAFRGKHLSFTVRFPNQGKEVEDLDILISHTWATIGS
                                                                                                                                                                                                                                                                                                                  AKLSQDWFPFLELLÄIALNPHCKFHVYNGARPCESVSSSVQFPEDELFACSPDLHSPK
GWLVDLINTFGTLNGFQILHDRFTSGSALNVQTIAAPIKPFGQCYEFLTQHTLRKYFI
PVIEVVPQILQKLTNEELKKETKTEVKNDTISMIIKFLKNLASRIPGQEETVKNLETF
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DLTKKGLDVKSEACQRFFRDVLTVSFSKILMDEAVSGWKFEIHRCIINNTHRLVELCV
                                        VRRCILNRMNVNVAHTKIELFIGGELVÄSEDDRKLVEQLNLKDKSLITÄKFIQINSNM
PSSPDSSSDSSAGPPONHSHNNYRDVSNPEMEKCLPGVIMSLQPRYISFLMQVADLGS
VLYLTEVVYTLLMPAGAPLADISSDFQYHFLKSGGLPLVLSMLIQNNFLPNTDVETRR
                     MLTVPTLRDGARILMKLMPPDSTTLEQLRALCSDHVNLGERRLGQSLHSLFFGSSASQ
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1. .8117
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/db_xref="taxon:10090"
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DEFINITION
ACCESSION
               Query Match:
                            Best Local
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                                                                                    Scores:
                           Similarity:
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Sequence 439 from Patent W00188188.
AX305688
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                            Ishikawa,K., Asai,S., Takahashi,Y., Naga
Method for examining ischemic conditions
Patent: WO 0188188-A 439 22-NOV-2001;
                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                            AX305688.1 GI:17645121
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EDPDDQDALDEHVSHAPQDRTFYLYSHRSHYQQNYVPEQPFSGPASHHLNNPQKNDKP
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KELLSFQSPEKKYHIGCKTGGANLVKELIDYFIFPASKAYLQYMRSGELPIKQAIPVC
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EDITETYKMTTSTRSNLEVKDEQVCCEALEVMTLCFALIPTAMDSLNKEKAWQSFVID
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                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
1989 c 2201 g 307
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                                                                                                                                                                                                                                                                                     Murinae;
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RESULT 27 AX305688

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Score: Alignment ORIGIN

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1 (bases 1 to 10323)
Wood,S.A., Pascoe,W.S., Ru,K., Yamada,T., Hirchenhain,J., Kemler,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning and expression analysis of a novel mouse gene with sequence similarity to the Drosophila fat facets gene Mech. Dev. 63 (1), 29-38 (1997)
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GWLVDLLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFL
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LLAFQTPEKKFHIGCEKGGANLIKELIDDFIFPASNVYLQYMRNGELPAEQAIPVCGS
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/db_xref="GI:1527199"
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/product="FAM"
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/chromosome="X"
/map="DMit53 - DMit57"
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|mol_type="mRNA"
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PATINAGFELLVALAVGCVRNLKQIVDSLTEMYYIGTAITTCEALTEWEYLPPVGPRP
PKGFYGLKNAGATCYKNSVIOQLYMIPSIRNGIAIEGTGSDVDDMSGDEKQDNESD
VDPRDDVFGYPQFENKPPLIKTENRKKYNIGVLKHLOVIFGHLAASRLQYYVPKGFW
KQSRLWGEPVNLREQHDALKSFNSLVDSLDEALKALCHPAMLSVLGGSFADQXICQG
CPHRYECEESFTTLAVDIRNHQNLLDSLEQYVKGDLLEGANAYHCEKCNKKVDTVKRL
LIKKLPPVLAIQLKRFDYDWERECAIKFNDYFFERDMEPYTVAGVAKLEGDNVNP
ESQLIQQNEQSESEKAGSTKYRLVGVUVHSGQASGGHYYSYIIQRNGGDGEKKRWYKF
DDGDVTECKWDDDEEMKTQCFGGEYMGEVLDHMMKRMYSYRQKRWMAAYILFYERMDT
IGHDDEVIRYISEIAITTRPHQIVMFSAIERSVRKONVQFMHNRMQYSLEYFQFMKKL
LTCNGVYLNPPPGQDHLSPEALEITMISIQLAAFFLCTTGFHTYKIVGSASGWYDAL
CILLRHSKNVRFWFAHNVLFNVSNRFSEYLLECPSAEVRGAFAKLYVFLFVMYANLGV
AEKTQLLKLSVPATFMLVSLDERGEPPIKYQYAELGKLYSVVSQLIRCCNVSSRMQSS
INGNPSLPRNPGDSQAYDNLSLSDHLFRAVLNLLRECPSAEVGRFAKLYVFNLALGF
AEKTQLLKLSVPATFMLVSLDEGFGPPIKYQYAELGKLYSVVSQLIRCCNVSSRMQSS
INGNPSLPRNPGDSNLSQPIMPIQQNVDBILFVRTSVKKIIEDSWQTHRINALKGIPD
DRDGLFDTIGASKNHYQKRAYGTKCMVALFSSCPVAXQILGCNGDLKKKWTMAVBUL
GDELERRFYTGNPQYTYNNMSPPVQSNETSNGYFLERSHSARMTLAKACELCPEEEPD
DQDAPDEHESPPPEDAPLYPHSPGSQYQQNNHVHGQPYTGPAAHHMNNPQRTGQRAQE
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Submitted (03-APR-2003) Genome Sequencing Center, Washington
                 Direct Submission
                                                              MO 63108, USA
                                                                          Submitted (30-MAR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                            Direct Submission
                                                                                                                                                                  Submitted (27-MAR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                  MO 63108, USA
3 (bases 1 to 26013)
Waterston, R.H.
Direct Submission
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Mar 27, 2003 this sequence version replaced gi:27819484.
                                                                                  Finishing Completed at Stanford Human www-shgc.stanford edu Quality: Phrap Quality >=40 100% of Se
                                                                                                                                                                                                                                                                     Submitted (22-JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 125439)
DOE Joint Genome Institute and Stanford Human Genome Center.
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On Apr 3, 2003 this sequence version replaced gi:29373197.
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AC138990
AC138990.2 GI:29294040
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               NOTE: This sequence is not the entire sequence of the clone (entire sequence is 153.5kb). It is clipped at the overlap with
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwate, K.J., Draper, H., Dugn, R.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Hamilton, K., Harris, C., Harris, K., Harr, M., Havlak, P., Hale, S., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jackson, D., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlyson, E., Karlyson, L., Korvah, J., Kovar, C., Karlyson, E., Klan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Martindale, A., Mei, G., Metzker, M., Massey, E., Mawhiney, E., McLeod, M.P., Martindale, A., Martinez, E., Moser, M., Norris, S., Oguh, M., Okwonu, M., Morris, S., Orasik, T., Pickens, R., Partmus, E., Pu, L.L., Quiles, M., Ren, Y., Soherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Soherer, S., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Warten, R., Washington, C., Wattingcon, S., Walliamson, A., Wleczyk, R., Wooden, S., Wang, O., Wang, S., Warden, R., Washington, C., Wattingcon, S., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43208 AAATACCATCATGCCCTATTAGCAAAAGTGGCAGTTGGGTTATCCTCA
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T. Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bimage,K., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 12 clone SEQUENCE, 4 unordered pieces. AC073440
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_D
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP13-708P15"
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Banks,T.,
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TITLE
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                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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ORIGIN
                                                                                                                                                                                                                       Score:
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AUTHORS
US-10-081-935-2 (1-18)
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Center clone name: RP11-100E14
Cente
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On Apr 28, 2002 this sequence version replaced gi:16117941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                            clone="RP11-100E14"
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2113: gap of unknown length
31789: contig of 29676 bp in length
31889: gap of unknown length
79584: contig of 47695 bp in length
79684: gap of unknown length
133445: contig of 53761 bp in length
                                                                      7.16e+03
46.00
93.75%
43.75%
56.10%
AC073440 (1-133445)
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                                                                                                                                                                                                                                                                                                                                                                                   25551 g 40640
                                                                                                                                                                                                     Length:
Matches:
                                                               Gaps:
                                                                                                    Mismatches:
Indels:
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REFERENCE
AUTHORS
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Best Local Similarity:
                        Query Match:
                                                                                                                                                                            BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 146757 bases at least Q40
Consensus quality: 146840 bases at least Q30
Consensus quality: 146855 bases at least Q30
Consensus quality: 146855 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 146908; sum-of-contigs estimation
Quality coverage: 15.57 in Q20 bases; agarose-fp estimation
Quality coverage: 15.57 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147008 bp Homo sapiens chromosome 5 clone SEQUENCE, 2 unordered pieces. AC138980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAla 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Project Name: 3069541
Center clone name: RPCI-13_169F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Direct Submission
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                48290
                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved
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                                                                                                                                                                                         /clone="RP13-169F15"
/clone_lib="RPCI human BAC library 13"
26527 c 25955 g 46136 t 100 oth
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
7.9e+03
46.00
81.25%
56.25%
56.10%
                                                                                                                                                                                                                                                                                                                                                   .147008
                                                                                                                                                                                                                                                                                                                                                                                     28773: contig of 28773 bp in length 28873: gap of unknown length 147008: contig of 118135 bp in length
Gaps:
                                        Conservative: Mismatches:
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RP13-169F15, WORKING
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AC138981
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         Alignment Scores:
                                                                        ORIGIN
                                                                                                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 146200 bases at least Q40
Consensus quality: 146424 bases at least Q30
Consensus quality: 146579 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 146777; sum-of-contigs estimation
Quality coverage: 5.31 in Q20 bases; agarose-fp estimation
Quality coverage: 6.33 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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2763
12053
12153
28942
29042
86683
                                                                                                                                                                                                                                                                                                                                                 1 2662: contig of 2662 bp in length
2762: gap of unknown length
2763 12052: contig of 9290 bp in length
2763 12152: gap of unknown length
2763 12152: gap of unknown length
2763 12152: gap of unknown length
2764 28041: gap of unknown length
2764 86682: contig of 57641 bp in length
2764 86782: gap of unknown length
2765 86782: gap of unknown length
2766 86782: gap of unknown length
2767 86782: gap of unknown length
2768 86782: gap of unknown length
                                                                                                      В
                                                                                                                                                                                            /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                /clone="RP13-193I10"
/clone_lib="RPCI human BAC library 13"
26217 c 26202 g 45840 t 401 oth
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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RP13-193I10, WORKING
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G DRAFT
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94598, USA
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KEYWORDS
SOURCE
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DEFINITION
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Best Local Similarity:
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76357
86396
94653
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64189
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US-10-081-935-2 (1-18) x AC138981 (1-147177)
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                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 161,624 genomic DNA of 18q21 published Only in DataBase (2000) 2 (bases 1 to 161624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7288187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer :::::: ||||||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP001493.2 GI:8117351
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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161624 bp DNA linear HTG
Homo sapiens chromosome 18 clone RP11-779H19 map 18g21,
DRAFT SEQUENCE, 23 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 161624)
                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: PCR products; 100% of reads Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 150399 bases at least Q40
Consensus quality: 155891 bases at least Q30
Consensus quality: 158205 bases at least Q20
Insert size: 159424; sum-of-contigs
Quality coverage: 5.50x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project Information
Center project name: HumDraft18
Center clone name: RP11-779H19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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46.00
81.25%
56.25%
56.10%
                                                                       32754 contig
48719 contig
64088 contig
76256 contig
                            86295
94552
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32754 bp
15865 bp
15269 bp
12068 bp
9939 bp
8157 bp
7943 bp
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WORKING
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110768 116555 contig of 5788 bp in length
112656 122099 contig of 5444 bp in length
122200 125461 contig of 3262 bp in length
122200 125461 contig of 3262 bp in length
131178 135924 contig of 5516 bp in length
131178 135924 contig of 2285 bp in length
136025 138309 contig of 2285 bp in length
140933 144613 contig of 3681 bp in length
140933 144613 contig of 3681 bp in length
140933 144613 contig of 3681 bp in length
150921 154114 contig of 3194 bp in length
150921 154114 contig of 3194 bp in length
154315 156288 contig of 3194 bp in length
156389 156442 contig of 3194 bp in length
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32855
48720
48820
/organism="Homo sapiens"
                                             Location/Qualifiers
                                                         135924: Contig of 4747 bp i
136024: gap of 100 bp
138309: contig of 2285 bp i
138409: gap of 100 bp
144613: contig of 2423 bp i
144713: gap of 100 bp
144713: gap of 100 bp
147780: contig of 2667 bp i
147780: contig of 2667 bp i
147780: gap of 100 bp
150920: contig of 3340 bp i
150920: gap of 100 bp
154114: contig of 3340 bp i
154214: gap of 100 bp
154318: contig of 304 bp i
1543214: gap of 100 bp
154318: contig of 2074 bp i
15438: contig of 2094 bp i
15438: contig of 100 bp
15438: gap of 100 bp
15438: contig of 2094 bp i
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15438: gap of 100 bp
156482: contig of 2094 bp i
156424: gap of 100 bp
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4: gap of 100 bp
9: contig of 15865 bp in length
9: gap of 100 bp
8: contig of 15269 bp in length
8: gap of 100 bp
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contig of 5444 bp i
gap of 100 bp
contig of 3262 bp i
gap of 100 bp
contig of 5516 bp i
gap of 100 bp
contig of 64747 bp i
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f 100 bp
g of 7972 bp
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of 8157
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FEATURES

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RESULT 35
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                      LOCUS
DEFINITION
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                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                              Pred. No.:
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AL391259 163520 bp DNA linear PRI 06-DEC-2001
Human DNA sequence from clone RP11-469E19 on chromosome Xp11.4-21.2
Contains a pseudogene similar to chloride intracellularnchannel 1
                                                                                       158583. .160442

/note="assembly_fragment"

160543. .161624

/note="assembly fragment"

a 30115 c 30590 g 49168 t
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32855. .48719
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/db_xref="taxon:9606"
/chromosome="18"
/map="18q21"
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L58583. .160442
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|54215. .156288
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136025. .138309
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.50921. .154114
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47481. .150820
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|40933. .144613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment clone_end:SP6 vector_side:left"
.38410. .140832
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|31178. .135924
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| 16656. .122099
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L10768. .116555
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102696. .110667
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Indels:
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Matches:
Conservative:
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REFERENCE
AUTHORS
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JOURNAL
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ORGANISM
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VERSION
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humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On Nov 23, 2000 this sequence version replaced gi:11322140.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/ChrX
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-469E19 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sections only once, except for a short overlap.
The true left end of clone RP51-469E19 is at 1 in this sequence.
The true left end of clone RP5-1051C18 is at 1185 in this sequence.
The true left end of clone RP5-1172N10 is at 163421 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-469E19 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-DEC-2001) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, the 5' end of the protease 9 (Drosophila fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pBACe3.6
                                                                                                                                                                                                                                                                                       408.
                                                     2490
                                                                                               /note="MLT1D repeat: matches 3.
2147. .2448
                                                                                                                                           /note="FRAM repeat: matches 0. .173 of consensus"
1923. .2107
                                                                                                                                                                                                                                        1462.
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11.2"
108. .615
                                                'note="AluSc repeat: matches 1.
1490...2647
                                                                                                                                                                                                           'note="MLT1D repeat: matches 217. .461 of consensus"
                                                                                                                                                                                                                                                         'note="AluJo repeat: matches 87.
                                                                                                                                                                                                                                                                                                                                clone="RP11-469E19"
                                                                                                                                                                                                                                                                                                                                                      map="p11.4-21.2"
                                                                                                                                                                                                                                                                                                                                                                                 'chromosome="X"
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                                                                                                                                                                                                                                        . 1669
                             repeat: matches 139. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USP9X gene for ubiquitin specific facets related) and a CpG island,
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                                                                       .302 of consensus"
                                                                                                                     .184 of
                                                                                                                                                                                                                                                            .286 of consensus"
                                                                                                                   consensus"
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9299. .9451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJo repeat: matches 17.
complement(2970. .3296)
/note="match: GSS: Em:AQ279697"
                                                                                                           /note="FLAM_A repeat:
,3184. .13491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSp repeat: matches 1.
7436. .7625
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                                                                                                                                                          /note="L1MC/D repeat: matches 5662.
13097. .13178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Charliela repeat: matches 1287. .1379 of consensus" 11039. .11322
                                                                                                                                                                                                        /note="Charliela repeat: matches 33.
12896. .13033
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSc repeat: matches 2.
11333. .11367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="54 copies 2
8520. .8657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6627. .6702
/note="LTR33 repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="FLAM_C repeat: matches 12.
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                                            note="LTR41 repeat: matches 13. .148 of consensus"
                                                                                                                                                                                                                                                                          note="FLAM_A repeat: matches 1. .115 of consensus"
                                                                                                                                                                                                                                                                                                                       'note="Charliela repeat: matches 381. .1104 of consensus"
                                                                                                                                                                                                                                                                                                                                                                     note="FRAM repeat: matches 2. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                 note="U2 repeat: matches 1. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Charliel repeat: matches 2161. .2574 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSx repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0256. .10557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="FRAM repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluSx repeat: matches 137. .286 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 3. .147 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 136. .312 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluJo repeat: matches 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSx repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note≃"AluJb repeat: matches 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Charlie1 repeat: matches 2593. .2756 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5872
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                                                                                        matches 5323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .146 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .191 of consensus"
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. 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .309 of consensus"
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                                                                                                                                    .109 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 143
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                                                                                     .5613
                                                                                                                                                                                  .5791 of consensus"
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of.
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US-10-081-935-2 (1-18) x AL391259
                                                     166876 bp DNA 1
Homo sapiens chromosome 1 clone RP5-1051C18,
PROGRESS ***, 26 unordered piecee
                                                                                                                                                                                                                                                                                  1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSer 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1PA11 repeat: matches 5718. .5849 of consensus" 19346. .19646 /note="AluSg repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER518
23550. .23861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSq/x repeat: matches 1. .120 of consensus" 21492 .21791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="42 copies 2 mer ta 65% conserved"
19835. .20139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSx repeat: matches 1. .166 of consensus"
19100. .19227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18833. .18998
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18468. .18553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="LTR41 repeat: matches 418. .453 of consensus" 14145. .14452 /note="AluJo repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LTR41 repeat: matches 148. .301 of consensus"
14112. .14144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19647. .19730
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21922. .22076
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15980. .16075
| Inote="MERSA repeat: matches 13. .112 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="AluSx repeat: matches 3. .297 of consensus"
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17479. .17743
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8, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 151580 bases at least Q40 Consensus quality: 156291 bases at least Q30 Consensus quality: 156291 bases at least Q30 Consensus quality: 159609 bases at least Q20 Insert size: 164376; sum-of-contigs Insert size: 184764; 6.6% error; agarose-fp Quality coverage: 2.91x in Q20 bases; sum-of-contigs Quality coverage: 2.72x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9214009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: dJ1051C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is
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Percent Similarity:
Best Local Similarity:
Query Match:

8.8e+03 46.00 76.47% 52.94% 56.10%

Alignment Scores:

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1: gap of 100 bp
4: contig of 3703 bp in length
7: contig of 11693 bp in length
7: gap of 100 bp
6: contig of 13759 bp in length
6: gap of 100 bp
3: contig of 5017 bp in length
3: gap of 100 bp
3: contig of 3015 bp in length
8: gap of 100 bp
9: contig of 2382 bp in length
9: contig of 68639 bp in length
9: gap of 100 bp
9: gap of 100 bp
9: gap of 100 bp
9: contig of 8639 bp in length
9: gap of 100 bp
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Muzny, D. Marie, Metzker, M. Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Ballen, C., Allen, H., Ayodeji, M., Baca, E., Baden, H., Balwalo, D., Bandaranaike, D., Barber, M., Byth, P., Brown, M., Belawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cree, A., D'Souza, L., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Duran, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farsaer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Gabisi, A., Ganta, R., Garcia, A., Garrer, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Handerson, N., Hernandez, J., Hadand, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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Rattus norvegicus clone CH230-255F21, WORKING DRAFT SEQUENCE, 6
unordered pieces.
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fragment_chain:7"
163750. .166876
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/note="assembly_fragment:00551"
114842. .118544
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fragment_chain:7
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149414. .152428
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155011. .163649
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152529. .154910
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130438. .144196
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|18645. .130337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23194840.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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3 (bases 1 to 169693)
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NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                      Center project name: GUVZ
Center clone name: CH230-255F21
Center clone name: CH230-25F21
Center name: CH230-25F21
Cent
                                                                                                              Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
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               l (bases 1 to 170270)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 170,270 genomic DNA of 18q21

Published Only in DataBase (2000)

Chases 1 to 170270)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                        AP001548.2 GI:8117386
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 18 clone RP11-83712
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NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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69386. .71663
/note="wgs_contig"
complement(88241. .88650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CH230-255F21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nd_sequence:BZ115992"
42528 c 43376 g 40890
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1763: gap of unknown length
162672: contig of 90909 bp in length
162772: gap of unknown length
164075: contig of 1303 bp in length
164175: gap of unknown length
165368: contig of 1303 bp in length
165368: contig of 193 bp in length
165468: gap of unknown length
166978: contig of 2510 bp in length
168078: gap of unknown length
168078: gap of unknown length
168078: gap of unknown length
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Indels:
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                    1 30841 contig of 30841 bp in length
30942 49995 contig of 19054 bp in length
50096 70667 contig of 20572 bp in length
70768 89290 contig of 1823 bp in length
105548 120373 contig of 1826 bp in length
1120474 133122 contig of 1826 bp in length
113043 147902 contig of 18279 bp in length
113304 147902 contig of 4599 bp in length
1143003 152506 contig of 4599 bp in length
115800 158705 contig of 4599 bp in length
115800 162039 contig of 3093 bp in length
116401 164114 contig of 2906 bp in length
1164120 1064114 contig of 2988 bp in length
1164121 166502 contig of 2479 bp in length
1164215 169081 contig of 2479 bp in length
1164215 169082 contig of 2479 bp in length
1164215 169082 contig of 2479 bp in length
1164215 170270 contig of 2479 bp in length
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1169182 170270 contig of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are unknown. This record will be updated with the finished as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:81-\tilde{4}2-77\tilde{8}-9\tilde{9}24)
On May 30, 2000 this sequence version replaced gi:7340850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HumDraft18
Center clone name: Rp11-83712
Center clone name: Rp11-83712
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 162012 bases at least Q40
Consensus quality: 162012 bases at least Q30
Consensus quality: 165830 bases at least Q30
Consensus quality: 167538 bases at least Q20
Insert size: 166670; sum-of-contigs
Quality coverage: 5.46x in Q20 bases; sum-of-contigs
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Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: RIKEN
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133153
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120373:
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70667:
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49995:
                                                                                                                                                                                                                                                                                                                                                              30841:
                                             gap of 100 bp

7 contig of 20572 bp in length

8 gap of 100 bp

9 contig of 18523 bp in length

9 gap of 100 bp

7 contig of 16057 bp in length

9 gap of 100 bp

10 contig of 14826 bp in length

10 gap of 100 bp

11 contig of 14826 bp in length

12 gap of 100 bp

13 contig of 14679 bp in length
                                                                                                                                                                                                                                                                                                    contig of 30841 bp in length
gap of 100 bp
contig of 19054 bp in length
  gap of contig
  100 bp
of 9951
bp in length
                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                     US-10-081-935-2 (1-18) x AP001548 (1-170270)
                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                    BASE COUNT
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                                                                                                                                                                          Score:
                                                                                                                                                                                               Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment"
|69182. .170270
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
164215. .166502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
|62140. .164114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment"
|58806. .162039
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143304. .147902
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/db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                      note="assembly
                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
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.55800. .158705
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.52607. .155699
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169181: gap of 100 bp
170270: contig of 1089 bp
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contig of 3234 bp
gap of 100 bp
contig of 1975 bp
gap of 100 bp
contig of 2288 bp
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32593 g 51749
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RESULT 39 AC090405

DEFINITION

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58369

ACCESSION VERSION

KEYWORDS

ORGANISM

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Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., McRernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., McRernan, K., McPheeters, R., Meldrim, J., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schuback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teffaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 27, 2001 this sequence version replaced gi:12958041. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 170413)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barren, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dear, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dear, K., Diaz, J.S., Dear, Dea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 170413)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-779H19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC090405 170413 bp DNA linear Homo sapiens chromosome 18 clone RP11-779H19 map SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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AC090405
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
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::::::|||:::|||:::|||
TTGAGGTTTACTCACTCTCTCTCTTCCCTTCTGCAGGCTGGAATGGCA 58322
                arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 165803 bases at least Q40 Consensus quality: 167767 bases at least Q30 Consensus quality: 167769 bases at least Q20 Insert size: 157000; agarose-fp Insert size: 169113; sum-of-contigs
                                                                                                                                                                Quality coverage: 8.9 in Q20 bases; agarose-fp Quality coverage: 8.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L12:
Center clone name: 779_H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
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                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                           BASE COUNT
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                                                                                                                                   Pred. No.:
                                                                                                                                                             Alignment Scores:
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39049. .43570
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/clone lib="RPCI-11 Human Male BAC"
1. .27912
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28013. .28759
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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34738. .38948
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|62271. .170413
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28860. .29596
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/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
|mol_type="genomic DNA"
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162170: contig of 118500 bp in length
162270: gap of 100 bp
170413: contig of 8143 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34737: gap of 100 bp
38948: contig of 4211 bp in length
39048: gap of 100 bp
43570: contig of 4522 bp in length
43670: gap of 100 bp
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COMMENT

JOURNAL TITLE JOURNAL REFERENCE

TITLE

AUTHORS

REFERENCE AUTHORS

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RESULT 40
AC134519
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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                                           Percent Similarity:
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ORIGIN
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      Query Match:
DB:
                                                                                                                             Alignment Scores:
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                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 173858 bases at least Q40
Consensus quality: 174094 bases at least Q30
Consensus quality: 174162 bases at least Q20
Estimated insert size: 174000; agarose-fp estimation
Estimated insert size: 174000; agarose-fp estimation
Quality coverage: 11.95 in Q20 bases; agarose-fp estimation
Quality coverage: 11.95 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Mammalia; Eutheria; Primates; Cal
1 (bases 1 to 174171)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
Center Project Name: 1547620
Center clone name: RPCI-11_659C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC134519
AC134519.1 GI:23334701
ATG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174171 bp DNA 1 Homo sapiens chromosome 5 clone RP11-659C12, SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-SEP-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 174171)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
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                                                                                                                                                                                       /clone="RP11-659C12"
/clone_lib="RPCI huma
30550 c 30653 g 5
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .174171
    9.39e+03
46.00
81.25%
56.25%
56.10%
                                                                                                                                                                                                                                                                                                                                                                        174171: contig of 174171 bp in length.
                                                                                                                                                                                ="RPCI human BAC library 11"
30653 g 57679 t
Conservative: Mismatches: Indels: Gaps:
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174171
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121346 AAATACCATCATGCCCTATTAGCAAAAGTGGCAGTTGGGTTATCCTCA 121393

Search completed: November 13, 2003, 12:34:37 Job time : 2171 secs

В

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Command line parameters:

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-MODEL=frame+_D2n.model -DEV=xlh
-Q=/cgn2__I/USPT0_spool/US10081935/runat_04122003_134829_10475/app_query.fasta_1.391
-DB=GenEmb1 -QFWT=fastap -SUFFIX=rge -WINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=40 -MODE=LOCAL
-UNTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US10081935_@CGN_1_1_2372_@runat_04122003_134829_10475 -NCPU=6 -ICPU=3
-NO_MMAP -LARGECUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Dugger, K.O. and Galgiani, J.N.
Direct Submission
Submitted (01-NOV-1995) Kris O.
University of Arizona, 1501 N.
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Cloning and sequence analysis of the cDNA for a Coccidioides immitis with immunogenic potential Biochem. Biophys. Res. Commun. 218 (2), 485-489
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Onygenales, mitosporic Onygenales, Coccidioides.

(bases 1 to 1201)
Dugger, K.O., Villareal, K.M., Ngyuen, A., Zimmermann, C.R., Law,
and Galgiani, J.N.
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                                                                         ProCysValGluGluAlaCysProLeuAspAlaArgIleSerValSerAsnIleValVal
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 GACCAGTGCTCCAAGGCCGGTGTCCCAATTGACATCCCACCAGTTGACACCACCGCCGCT
                                                        CCTTGCGTTGAGGAGGCCTGCCCTCTCGACGCCCGTATCTCCGTCTCCAACATCGTCGTT
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PTASTPAEFPGAGSNVRASVGGIAAALLGLAAYL"
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/mol_type="mRNA"
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Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 1334)
                                                                                                                                                                                                                                                                                                                                                        Submitted (27-JUL-1995) Texas Research Immunology, 2303 S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhu, Y., Yang, C., Magee, D.M. and Cox, R.A. Molecular cloning and characterization o antigen 2 cDNA [Infect. Immun. 64 (7), 2695-2699 (1996)
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Coccidioides immitis antigen
U32518 GI:1200179
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M Coccidioides posadasii

Coccidioides posadasii

Eukaryota; Fungi; Ascomycota; Pezizomycotir

Onygenales; mitosporic Onygenales; Coccidic

1 (bases 1 to 1435)

Zhu, Y., Yang, C., Magee, D.M. and Cox, R.A.

Coccidioides immitis antigen 2: analysis of

Gene 181 (1-2), 121-125 (1996)

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   Submitted (12-MAR-1996) Rebecca A. Cox, Clinical Investigation, Texas Center for Infectious Disease, 2303 S.E. Millitary Dr., San Antonio, Ty 78223, USA Location/Qualifiers
                                              2 (bases 1 to 1435)
Zhu, Y., Yang, C., Mag
Direct Submission
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PSETARPTAEPTEPTAEPTAEPTAEPTAEPTEPTAVPTGTGGGVPTGTGSFTVTGR
PTASTPAEFPGAGSNVRASVGGIAAALLGLAAYL"
a 414 c 327 g 361 t
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|mol type="genomic DNA"
|strain="Silveira"
|db xref="taxon:199306"
|join[175. .255,334 . .472,575 . .939
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Direct Submission

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2 (bases 1 to 3821)
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Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 3821)
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Dean,R.A. Dr. Mitchell,T. Dr.
Direct Submission
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Magnaporthe grisea
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1316 GACCAGTGCTCCAAGGCCGGTGTCCCAATTGACATCCCACCAGTTGACACCACCGCCGCT
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Submitted (11-JAN-2002) Plant Pathology - Fungal Genomics Laboratory, North carolina State University, 840 Main Camp Raleigh, NC 27606, USA
* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (Dases 1 to 97478)
Dean,R.A. Dr, Mitchell,T. Dr, Thon,M. Dr, Brown,D.E., Taro,A.
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13062: contig of 8150 bp in length
13162: gap of unknown length
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134712: contig of 21550 bp in length
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Mamestra
AY057052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-SEP-2001) Molecular Genetics, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Lepidoptera; Glossata; Dit Noctuoidea; Noccuidae; Hadeninae; Mamestra.
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Mamestra configurata
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                                                                             AspIleProProCysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAspGlyCysThr
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AQACDWPFNVPHCAGSAGATAAPTTEADSEEIPLPNDPDSWESLPNGCPVDSSISHLV
PHESDCDKYYVCDNGRLVQLGCPAGTHESPSQQFCTWPHEAGCEHWTGGGCTTPGNGG
GSCGGSTAAPVDPTTPVAVVTSTSAPISPSTSAPNEPSTPVAVVTTTTSAPISVPST
SAPNDPTTPVAVVTSTSAPISPSTSAPNEPSTPVAVVTTTTSAPISVPST
SAPNDPTTPVAVNSSEEIPLPNDPEDLLPNGCPADFEVDLLLPHETDCDKFYYCVHGEI
VEFPCAPGTHFSPALQACTWPQEAGCEHWSEPSTVAPEITVTAVTSTLSVAPDTTAAV
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/protein_id="AAL17912.1"
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'db_xref="taxon:174822"
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Hegedus,D.
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Bj.o slashed.rnvad,M.Eskelund., Hatakeyan
Nielsen,J.Bech.
Endo-B-1,4-glucanases from saccharothrix
Patent: US 6207436-A 1 27-MAR-2001;
Location/Qualifiers
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Rivailler, P., Cho, Y.G. and Wang, F.
Complete genomic sequence of an epstein-barr virus-related herpesvirus naturally infecting a new world primate: a defipoint in the evolution of oncogenic lymphocryptoviruses J. Virol. 76 (23), 12055-12068 (2002)
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Callitrichine herpesvirus 3
Viruses, dsDNA viruses, no RNA
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Rivailler, P., Cho, Y. and
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Boston, MA 02115, USA
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Sequence update by su
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FETULLWCLLIAWMNVTREDEPVSGRRSSMSSLSVAASTATAWRASFLTLSFOGLGLLLL
FGTALVIQTIYVLYLVWEITVMIMMERYLHFWITLLFLLSPFILSVACLIIOSSALL
IEAVVVTTITVUAIFLMLPPQGAEADIGTALLILNTALCLVVLILTAIPTDAQILTVF
CLFCQWTLFICLGIRMICNWRGKLTRIICLKFCLYGLISASLSFGWYAFLKEVTLPTT
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139106. 139219,139294. 139458,139572.
139744. 139992,140075. 140167,140247.
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/mol_type="genomic DNA"
/strain="CJ0149"
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Location/Qualifiers
                                                                                                                                                                                                                                                 /product="C7"
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                          specific_host="Common marmoset"
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                                                                                                                                                                                                                                                                                                                                                           xref="taxon:106331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              herpesvirus
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Channing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicine, Brigham & Women's Hospital, Channing Laboratory, 181 Longwood Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brigham & Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                         herpesvirus
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CJ0149,
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complete
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, 181 Longwood Ave
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gene

mRNA

SdC

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RALTSLAVAYARRNIPGDSENAGLLLVGFAEFLCLYRRAWLSRLGGIRVGLRRAFPLT
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VKPLLSGMICASGITMLVLGVVLLVVCTRASTRESIYEDLRYPTRDANGEYENVGYPP
RDGDAPHRLGEPVYDDVEQAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWRNPEEEDNRKQDRLGTKPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1564.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(484. .721,811. .897,1087.
/gene="C1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBV BALF3; transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .897,1087. .1829)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to bcl-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1829)
Query Match:
DB:
                                                                                   Best Local Similarity:
                                                                                                                                                                           Score:
                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                          Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SdC
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                                                                                                                                                                                                                                                               Scores:
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CDS

CDS

Sg

Gaps:

Conservative: Mismatches: Indels:

Matches:

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RGPEPPLOCHMORTS (OVMSHED) GROUND KKKCSANDGCAYEATOMEFHVYDI IETVYT

QEKCANI PSDKOGYVVPCGI U KLLGRRREDGASVCI NVFGOQGY FYSET PADVNI EV

ALVEI LKGGTFDRRT FCRMAVET VERRSI MGYGKTKKMYKI TLSHPNSI SHAATSIK

DKYGCKI FEANVDASRRFVLDKKTTTFGWYRCGROTKKMYKI TLSHPNSI SHAATSIK

DKYGCKI FEANVDASRRFVLDKKTTTFGWYRCGROTKKMYKI TLSHPNSI SHAATSIK

VIGNDVSWPPYNWARDI ECLGEEGFPNATNETDLI I QSVLMSVGEPTSNYRRI LL

TVGTCAE I DGVEVYEFPSEMDLI YA FF FOLI DLDKVEI I TGYNVANFDWPY I LDRARHI

YGINPASLGKI RGGGVCEVRRENDAGKWFSRACTKI RI SGVI PI DMYSVCKEKISLSD

YKLDTVAKRI LGTKKEDVHYKBI PHLFRAGPEERKRLGMYCI ODSVLVMDLLNHFVTH

VEI SEI AKI ANI PCRRVLDDGQOI RVFSCLLAAAQKEGEI LPMPEPSDROGYQGATVI

QPI AGFYNSPYLVVDBASLY PSI I QAHNLCYSTI VTGGEGKLABLERGEDY SEISGLS

GGTFHFVKKHI HKSFLAS LLESWLAKRKA I RKLLGACND PRORTI LDKOQLA I KCTCN

AVYGFTGVAHGLFFCLTI AGTVTLAGRTWLERAKVFVENLSLTDLEKLAPCSATPWSF

NPDGILIRUY VGOTDSLFI ECSGGFSEBOVSALSBPLARFTTSSLFNAP I SLEERKI FSC

LMLI TKKRYVGVLTDGKI TMKGVDLVRKTACQFVQTRCRRVLDLI LGNDKVKRAAS I L

SLRPYQTSTTGCLPEGFLDVINVLNBAYGDLARANRUP I SELSFTTELSRQI SAYKSTQ

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SLRPYGTSTGCLPEGFLDVINVLNBAYGDLARANRUP I SELSFTTELSRQI SAYKSTQ

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NVMFTGIIAATCWLLLAAPLVFRPEPGNLGFFCPSSLMTRYVHAFGSLLILLLLLLYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDEKALTVALRPASGI STGURRYNSOPDLYDDPGWAVWTYRRRTTVACMI TDMOAKSN SPENFFYTTLGGTVEMSPFYNGSNSETFNEPAGTE IR REKYK UT FEBRRGT I PREEKR AFLINKDTYILSWKLDARSSYCPLTMWKDYSVAI RTDDGSSFHF I TPOGTASFYTNTTH EKLPDOFKGI EQQVINKTI TEOFAKLSINKYDRDEAEI OYFRTAGGLLLAWLPVTPKSLI TIRD ALINNTEAQDGKAARDOFDTANST TPOAPPLRRNREASGDRITTIN ITOVSAT TEGFÖDKDSI LGTINDHADATAQI OFA VIDSLRSOJINKIJGDLASAWCOBERRONWYLINGTURD TROADSTINGTYNGYYYDPAARRI GDVI SYSRCYPVEGESVSLRKSMRVLGSETSCYTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAHRQFIDDLKNILESTLVSFRRASNPNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSFSFPNDSKTYEGOLGOFNEILLTKKMVENCODTCOHYFOSGNEMHVFRDYOHFKT
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ISKOOLDAIMLALYEOTAKRTOAESKTSDSTTSLPSRALEAARNRLRLRKKPGRENRS
DLKPLLTNIEDTEF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIAVEHYFEKLLQGTANILQCLFGNNPETALSVLQNFTAGYPHQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPHLIVYQKILARNEEPPQIHDRIPYVFVASAEGGRSGRGTRKSEMAEDPSYVTRHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIALRYWGDTYYEEMAAMYNHFIARRAFPHRAWEDKRDGTAEIFENSKYIKTHLFNOT
LSSEHVNALTMTYYSLLTGPLIGDAGMFPPBNNALSYSCEAAGILPHOKLFMASLVW
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DEAGLEGAVPPDGIYITYESENPLILILKTKGWIFKDLYALLYMHLQMVQDGRV"
                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to"
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/db_xref="GI:13676647"
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/product="ORF6"
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A Dictyostellum discoideum cellulase is a member germination-specific gene family
J. Biol. Chem. 266 (23), 15432-15437 (1991)
91332071
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Dictyostelium discoideum
Dictyostelium discoideum
                                                                                                                         Draft entry and computer-readable In press] kindly submitted by H.L.Ennis, 17-APR-1990.
                                                                                                                                                                                                                                                                                                                       Giorda,R., Ohmachi,T., Shaw,D.R. and Ennis,H.L. A shared internal threonine-glutamic acid-threo defines a family of Dictyostelium discoideum sp
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                                                      /organism="Dictyostelium
/mol_type="genomic DNA"
/strain="AX-3"
/note="spore germination-specific protein"
/codon_start=1
                           /db_xref="taxon:44689"
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                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Notudide; Plusiinae; Trichoplusia.

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Wang, P. and Granados, R.R. Molecular cloning and sequencing
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                                                      CCAACCACTGTCACAGTACCACCTÁCTGCTGCTCCCACCGCAGCCCCTACTACTGCTGTC
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                                                                                                                  CCTACTCCGGCCCCACCGCTGCCCCCACCGCAGCTCCTACTACTGCTGCCCCCTGAATCC 1696
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NFEIDWLLPHGNRCDKYYQCVHGNLVERRCGAGTHFSFEDQCDHIELVGCTLPCGES
EEVDVDEDACTGWYCCTEPIEWEPLPNGCPADFSIDHLLPEDQCGCYLCCVHGOTIA
RPCPGNLHFSBATQSCESPVTAGCQVFECDSDNQCTSTAAPTAAPTAAPTAAPTAAPT
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Invertebrate intestinal mucin cDNA and
Patent: US 6187558-A 1 13-FEB-2001;
Location/Qualifiers
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1 (bases 1 to 2821)
Wang, P. and Granados, R.R.
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Granados,R.R. and Wang,P.
Invertebrate intestinal mucin cDNA and related products and methods
Patent: US 6187558-A 2 13-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Unknown
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                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (20-NOV-2001) Zverlov V
Technical University of Muenchen,
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Zverlov, V.V.
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GTTTTCGAGTGCGATTCTGACAACCAGTGCACATCGACTGCTGCCCCGACAGCTGCTCCA 1510
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Fuchs, K.P
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US-10-081-935-4 (1-194) x CTH420770
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l (bases 1 to 3067)
Zverlov, V.V., Fuchs, K.P. and Schwarz, W.H.
Chil8A, the endochitinase in the cellulosome
cellulolytic bacterium Clostridium thermocell
Appl. Environ. Microbiol. 68 (6), 3176-3179 (
                                                                                                                                          Clostridium thermocellum
Clostridium thermocellum
Bacteria; Firmicutes; Clostridia; Clostridiales;
                                                                                                                                                                                                                    Z68924.2 GI:17977822
ChiA gene; chitinase;
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    cellulosome of the m thermocellum 3176-3179 (2002)
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Submitted (27-JAN-1996)
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revised by [3]
3 (bases 1 to 3067)
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On Dec 23, 2001
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Location/Qualifiers
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Birren, B., Linton, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camacata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Colling S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Petrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Medrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connot, T., O'Donnell, P., O'Neil, D., Rymond, C., Retta, R., Rieback, R., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Topham, K., Travers, M., Traillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Mus musculus (house mouse)
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Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Maddonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Myyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.,
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Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is available and the accession number will be preserved.

1 799: contig of 799 bp in length 800 899: gap of 100 bp 900 1664: contig of 765 bp in length 1665 1764: gap of 100 bp 1765 8745: contig of 6981 bp in length 8746 8845: gap of 100 bp 1765 8745: contig of 69756 bp in length 1765 8745: contig of 69756 bp in length 1765 8745: contig of 69756 bp in length
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------ project Information
Center project name: L24637
Center clone name: 220_A_11
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                       58207: contig of 14490 bp in 58307: gap of 100 bp 84732: contig of 26425 bp in 84832: gap of 100 bp in 115302: contig of 30470 bp in 115402: gap of 100 bp 169837: contig of 54435 bp in 169937: gap of 100 bp 207870: contig of 37933 bp in
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33647: gap of 100 bp
43617: contig of 9970 bp in length
43717: gap of 100 bp
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2 of 3 Caldicellulosiruptor sp. Rt69B.1
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169938. .207870
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115403. .169837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-220A11"
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Bacteria; Firmicutes; Clostridia; Clostridiales;
Syntrophomonadaceae; Caldicellulosiruptor.
1 (bases 1 to 5437)
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Morris,D.D., Gibbs,M.D.,
Direct Submission
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ENTIKLFSSIPGLEIHTTELDWSFYQWGSSTSYSTPPRDLLIKQAMRYKELFDLFKKY
NVITNVTFWGLKDDYSWLSQNFGKSDYPLLFBORYKSKYAFWSLIETVVPVNYSTLAF
PPAIQVPTPTSTPTPTVEATPTPAPTASPAGGSYWTPSESYGALKUWYANGNMS
STTNVLNPKIKIENVGTTAVDLSRVKVRYWYTIDGEAAQSVSVASSINPAYIDVRVVK
LGANAGGADYYVEVGFKSGAGVLAAGQSTKEIRLSIQKSSGSYNQSNDYSVRSANSYI
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AVAEVLPQSGSSSQWVKVEANVENVTGVHDLYLVFRGEKKSNLFDMDCWRFVR"
                                                                                                                                                                                                               TARVLQPGDDMISVVGSAATIPAPYMFEDSGINKIGNTYYYSYCTNFAQRPQGSPPAG
AIAYMTGKSPVGPWEYRGVILRNPGNFFGVGGNNHHQLFEFNGKWYIAYHAQTLAKDL
GVAKGYRSPHINQVQIENGVIKEVTADYKGVAQVKNFDPYRMVEAETFAWCAGISTKK
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RVKVRYMYTIDGEATQSVSVASSINPAYIDVRVVKLGAAAGGADYVEVGKFKSGAGVL
AAGQSTKEIRLSIQKSSGSYNQSUNDSVSVRSANSYIENEKVTGYIDDULVMGKEPSGT
KPAGEVTPAPTPTSTTTPAPTSAPTPSPTVTATPTPTPTPTATPTPTTTTP
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SELLISENNYNFSKADEFVNFATSNNIAIRGHTLVWHEQTPDWFFKDANGNTLSKDAL
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IVESGVDYNVDYIQIMDDNSYLSNAVTFSSGFESGTTEGWQARGSGVTVKPDSVVAYN
GKYSLYVSGRTSNWHGAQIPVDTILEQGKVYKISVWVXQNSGSTQKMSLTMQRRFATD
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65..5404
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/trans1_table=11
/producT=-ffamly 10 xylanase"
/protein id="AAB95326.1"
/db_xref="GI:2760909"
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/mol_type="genomic DNA"
/strain="Rt69B.1"
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/EC_number="
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Pneumocystis carinii f. sp. muris
Eukaryota; Fungi; Ascomycota; Pne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-SEP-1998) Microbiol. Med. & Dent., Box 672, 601 Elmwood
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Haidaris,C.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular characterization of KEX1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pneumocystidaceae; Pneumocystis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlySerPheThrValThrGlyArgProThrAlaSerThrProAlaGluPheProGlyAla 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProThrGluGluProThrAlaValProThrGlyThrGlyGlyGlyValProThrGlyThr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCACACCTGCACCGACATCAGCCCCGACACCGAGCCCAACAGTGACAGCAACGCCGACT 3277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGluProThrHisGlu 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGCGGGTGAAGTGACACCGGCACCGACGCCGACATCAACGCCAACACCGACACCTACA 3217
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/translation="MVYKIFLAFFLCWIFLIRVKSEEKPKDFENKDYYHFHFSKDVDL
DAFSQELGFBYEEALEHLDGHYLFSIDKGVSDDKIEEKIKDYFGLEGNIJGFNSDKL
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CAEGSYDFNTQTSDPSPKRSDDTHGTRCAGEIVAAKNTFCGVGVAYDAKVSGIRFLAS
VLSSWLEGKALSYRYDINDIYSCSWGPRDDGKTIEGVPYSAYNSIINGINLGRKGLGS
                                                                                                                                                                                                                                                     subtilisin-like
                                                                                                                                                /codon_start=1
/product="kexin-like protease KEX1"
/protein_id="AAF:2493.1"
/db_xref="GI:6958206"
                                                                                                                                                                                                                                                                                                                            /gene="kex1"
10. .3045
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                                                                                                                                                                                                                                                                            note="similar to
                                                                                                                                                                                                                                                                                                    'gene="kex1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="forma specialis: muris
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sp. m
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Ave., Rochester, NY 14642, L
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ACCESSION
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AC128838/c
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chen, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 ProThrGluGluProThrAlaValProThrGlyThrGlyGlyGlyValProThrGlyThr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 ProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGluProThrHisGlu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 GlySerPheThrValThrGlyArgProThrAlaSerThrProAla 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC1288383 G1:25073624
AC128838.3 G1:25073624
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC128838 256635 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-395E20, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 256635)
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DLTKTQSIVYPFIIRSSSIP GEBTVYLDTESATIESYSSQPTSESTSEPTPOPTPQ
PTPQPTSEFTSETSETSTSTKSPTDPTQQTSEETSESTSEPTSEPTPQPTPQ
PTPQPTSEFTSETSETSEPTSEPTSEFTSEFTSEPTSEPTPQPAPPQPAPPQ
PAPQPAPQPAPQPAPQPAPQPVPQPVPQPAPQPAPKFTPQPTSEPAPQPTSE
STSEFTERPPPQFVPSEPTSEFTSEFTSEFSEPSFPQPVPQPAPQPAPRKPAPKPTPPK
PAPKFTPPKPAPKPAPKKAPSKSSKTTSTSSSFISSTKKTTTQKASFTSASGRSSTQS
ASHTSFFKRULLLISILLASIILLIFGFLFLFIRFFKKRDSYTNGHPVTETLNYESDP
NMSQETEKATMLKRNQQVTSSDLSDTEDPNMYERRILKS"
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TNARIYTTDVGEKGCSTVHSGSSASTPIAAGVIALVLSVRPNLTWHDIQGLIVESAVP
FSLDYPGWEKLPSGRYYHYTFGYGKLDAYRMVEAARNFKHLNPQARESVPMIIYNKKF
SENNGHITDKFNLIKAYPDYNFGKLERVSVTLYFQHAKRGSLEINITSPSGVTSMLT
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TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Center project Information
Center project name: KAVH
Center clone name: CH230-395E20
Center clone name: CH230-395E20
Center clone name: CH230-395E20
Center clone name: Phrap; version 0.990329
Consensus quality: 199691 bases at least Q40
Consensus quality: 203386 bases at least Q30
Consensus quality: 203850 bases at least Q20
Estimated insert size: 203171; sum-of-contigs estimation

coverage:

6x in Q20 bases; sum-of-contigs estimation

Center: Baylor College of Medicine Center code: BCM Contact: hgsc-help@bcm.tmc.edu Web site: http://www.hgsc.bcm.tmc.edu/

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KEYWORDS SOURCE

REFERENCE

AUTHORS

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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J
                                                                                               District (12 Nov 2002) Number Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23915267. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 256635) 3 (bases 1 to 256635) Rit Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
GluProThrAlaGluProThrAlaGluProThrHisGluProThrGluGluProThrAla 139
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                                                            TCATCCATGGCATCATCCATGGCATCATCCACTGCATCACCCACTGCGTCACCCACTGCG
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                                                                                                                                                                                                                                                                                             GAACTGCATCATTGTÄCÄTTATGCATTATCTGTGCCTCACCCACTGCATCACCCATGGCÄ 87454
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58930. .61273
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kulkarni,R.D. and Dean,R.A. Identification of proteins interacting with adenylate cyclase and cAMP-dependent protein kinase A in the rice blast fungus
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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ptigcsgtdfkcqcqqqakmfaavescvqkscpesefqktidgsdkvctcasggpasn
naggagntvnpssfipgptstasptttvaaptgtpsgrpsavptaaanmaavecsivv
                                                                                                                                                                                                                                                                                                   GAVGGALWVALGL"
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/protein_id="AAN64312.1"
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Submitted (24-JUL-1998) Biochemistry, Universitaire, Ste-Foy, Que GIK 7P4, (Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

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               /db_xref="ATCC:32354"
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515. .4126
                                                                                                                        /organism="Candida albicans"
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2762. 3067
2762. 3067
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4067. 4123
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/note="encodes putative GPI-anchoring determinant"
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2207. .2512
/gene="CSA1"
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515. .565
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/trans1_table=12
/product=-mycelia1 surface
/protein_id="AAC29486.1"
/db_xref="GI:3406798"
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515. .4126
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/gene="CSA1"
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1211. .1516
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REFERENCE AUTHORS TITLE

KEYWORDS SOURCE ORGANISM

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JOURNAL REFERENCE AUTHORS TITLE

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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 4792)
Braun, B.R. and Johnson, A.D.
TUP1, CPH1 and EFG1 make independent contributions to filamentat:
in candida albicans
Genetics 155 (1), 57-67 (2000)
                                                            Braun, B.R. and Johnson, A.D.
Direct Submission
Submitted (11-APR-2000) Microbiology,
Parnassus Ave, S-410, San Francisco, (
Location/Qualifiers
                                                                                                                                                                                                    2 (bases 1 to 4792)
Braun, B.R., Head, W.S., Wang, M.X. and Johnson, A.D.
Identification and characterization of TUP1-regulated
Candida albicans
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/organism="Candida albicans
/mol_type="genomic DNA"
/db_xref="taxon:5476"
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ORIGIN
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gene
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SINGFADRI YDDOLPECAKPCMFQNTGVTPCPYWDTGCLCIMPTFAGAIGSCI AEKCKG
QDVVSATSLCTSI CSVAGVWDPYWMYPANVQSSLSAATAAVASSSEQPVETSSEPAGS
SQSVESSQPAETSSSEPAETSSSEPAETSSETSSEDOPASSEPAETSSEESSTITSAPS
TPEDNPYTI YPSVAKTASI NGFADRI YDQLPECAKPCMFQNTGVTPCPYWDTGCLCIM
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SSSTTTSTFI FITASI NGFADKLYDQLPECAKPCMFQNTGITPCPYWDDAGCLCVMPQFA
GAIGSCVADSCKGQDIVSATSLGTSVCSVAGVNAPYWMLPASVKSSLSVAATAVPTSD
SASETNAGQEPSETSSEQPSETASQQPAETSSEESSTITSAPSTPEDNPYTI YPSVAKT
ASINGFADRI YDQLPECAKPCMFQNTCYTPCPYWDTGCLCIMPTFAGAIGSCI LEKCK
GQDVVSATSLGSSI CSVAGVWDPYWMLPANVQSSLNAAATAVATSDSASEVASASSA
SQVPQDTSAASSQSANNSVASAAPSNASSVSAAPSSNASGVAPARSNNSSGASVVPSQS
ANNSSASAAPSNNSSSAI ESSVAPSNSSVSAAPSSNSGVAPARSNNSSGASVVPSQS
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CESSIOSI ESVKTSAEAHKTEVI ASCASELSSLSSAKSEAKKTVSSLVEVOKSAVAK
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QTSLAAVGSSAASVQLSAAANANANTEVATA TAMABNITEVATA TAMABNITETATA TAMABNITETATA TAMABNITETATA
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/gene="WAP1"
1175. .4231
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/note="contains predicted signal sequence and GPI addition
sequences, indicating localization in the cell wall;
sequences, or contains four cysteine-rich repeats similar to the single
contains four cysteine-rich repeat of Rbt5p and to Coccidioides imitis proline-rich
antigenic protein PRA; Waplp"
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/db_xref="GI:9963992"
                                                                 GKETGVSQATVAANTHSVAIANMANTKFASTMSLLVASFVFVGLFI"
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0.624 165.50 38.69* 24.62* 16.18* Length:
Matches:
Conservative:
Mismatches: Indels:

4792 49 28 89 33

US-10-081-935-4 (1-194) x AF254147 (1-4792)

TCTCAACCTGCTGAAACCTCATCATCTGAACCTGCTGAGACTTCATCATCTGAACCTGCT 1732 AlaLeuG|yAsnAspGlyCysThrArgLeuThrAspPheLysCysHisCysSerLysPro 53 AlaGluProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGluProThr 130 ATGGTGCCTGCAAATGTCCAGAGCAGTTTAAGTGCTGCTGCCACTGCTGTTGCATCGTCT 1612 SerValSerAsnIleValValAspGlnCysSerLysAlaGly-------ACATTTGCTGGTGCCATTGGTTCTTGTATTGCTGAGAAGTGTAAAGGCCAAGACGTTGTT 1492 AACACTGGTGTGACCCCATGTCCA---TACTGGGATACTGGGTGTTTGTGTATTATGCCA 1432 GlyLeuAlaSerAlaGlnLeuProAspIleProProCysAlaLeuAsnCysPheValGlu 33 TCTGCTACAAGTTTGGGAACTTCCATTTGTTCCGTTGCTGGTGTGTGGGGATCCATACTGG 1552 GluLeuProGlyGlnIleThrProCysValGluGluAlaCysProLeuAspAlaArgIle 73 ---ValProIleAspIle-----TCTGAACAACCAGTTGAAACATCTTCTGAACCAGCTGGATCTTCTCAGTCTGTTGAATCT -----ProProValAspThrThrAlaAlaProGluProSerGluThrAlaGluProThr 110 1672 87

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   Anyalebechi, V. Aoyagi, A. Ayodeji, M., Baca, E. Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Burker, M., Barnstead, M., Benahmed, F., Cardensa, V., Carter, K., Cavazosi, I., Casasri, H., Center, A., Chacko, J., Ccharer, E., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checko, J., Charer, R., Cayazosi, I., Casasri, H., Canter, A., Duchin, K., Duval, B., Eaves, K., Davis, K., Darper, H., Dugan-Rocha, S., Dunn, A., Duchin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falla, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Gebregergis, E., Geer, K., Gill, R., Grady, M., Garner, T., Garza, M., Gebregergis, E., Geer, K., Gill, R., Grady, M., Garner, T., Garza, M., Gebreger, C.M., Gabisi, A., Gandara, R., Garcia, A., Garner, T., Garza, M., Gebreger, C.M., Hadan, S. L., Hodgson, A., Hernandez, J., Harvey, Y., Havlak, P., Hadan, S. L., Hodgson, A., Hernandez, J., Hernandez, R., Hinges, S., Hladun, S. L., Hodgson, A., Hongues, M., Hernandez, J., Liu, Y., London, P., Longacre, S., Lopes, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lux, M., J., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopes, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lux, M., Malloy, K., Martin, K., Martin, R., Pal, S., Parks, K., Pascennak, S., Pull, H., Mendold, M., Malloy, K., Mangum, A., Mangum, A., Sodergren, E., Solter, M., Richards, S., Scott, G., Shatsman, S., Shen, H., Shen, J., Wallson, R., Wallson, R., Wallson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1847 TACACCATCTACCCAAGTGTTGCCAAGACT-----GCTTCTATCAATGGTTTTGCT 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1793 TCAGAAGAATCTTCTACAATCACTTCAGCCCCA----TCAACTCCTGAAGATAACCCA 1846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GlyThrGlySerPheThrValThrGlyArgProThrAlaSerThrProAlaGlu-----
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AC095003
AC095003.7 GI:30467553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Zhou, J., Zhou, X., Zhao, S., Dunn, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG 09-MAY-2003
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AUTHORS
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence rontigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence es as soon as it is available and the accession number will

* be preserved.
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Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 238046) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Niederhausern, A., Weiss, R., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Atlas;
Consensus quality: 226044 bases at least Q40
Consensus quality: 227924 bases at least Q30
Consensus quality: 229373 bases at least Q20
Estimated insert size: 234613; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GBYH
Center clone name: CH230-6K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
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6066._.6753
                                                                                                                                                                                                                                                                                                     clone="CH230-6K12"
                                                                                                                                                                                                                                                                                                                                        organism="Rattus norvegicus"
|mol_type="genomic DNA"
|db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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                                                                                                                                                                                                                                                                            .1680
                               sequence:BH360832'
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RESULT 24
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhay, C., Burch, P., Burcell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, J., Chacko, J., Chavez, D., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Devila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fersser, C.M., Gabisi, A., Ganta, R., Garreta, A., Garner, T., Garza, M., Gebbregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACO98905 225849 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-163J19, WORKING DRAFT SEQUENCE, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 225849)
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clone_end:Sp6"
235657. .23682
/note="wgs_end_extension
clone_end:Sp6"
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a 49774 c 51497 g 67565 t
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229310. .230352
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clone_end:Sp6
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32
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3
                                                   Foster, P.,
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least least least Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information

Center project name: GIOC

Center: Baylor C Center code: BCM

Genome Center

College of Medicine

Gunaratne, P., Hasland, W., Hamil, C., Hamilton, C., Hamilton, K., Harrey, Y., Havlak, P., Hawes, A., Herderson, N., Hernandez, J., Hernandez, R., Hines, S., Hlddin, S.L., Hodgeon, A., Mogue, M., Hernandez, H., Hosells, S., Hlddin, S.L., Hodgeon, A., Mogue, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, B., Johnson, B., Johnson, R., Johnson, R., Johnson, M., Johnson, B., Johnson, M., Johnson, M., Johnson, B., Johnson, M., Johnson, B., Johnson

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RESULT 25
                                                                                         ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
Dictyostelium discoideum Dictyostelium discoideum Eukaryota; Mycetozoa; Dic 1 (bases 1 to 4675)
                                                                                                            protein-like
U20608
                                                                                                                      Dictyostelium discoideum unknown protein-like protein, orf1, orf2
                                                                                         U20608.1
                                                                                                                                                              DDU20608
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                                                                                                                                                                                                                                                                                                                                                                                                                GluProThrAlaGluProThrAlaGluProThrHisGluProThrGluGluProThrAla 139
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                                                                                                                                                                                                                                    CAACCAACC---AACCAACCAACCAACCAACCA 211148
                                                                                                                                                                                                                                                                       ArgProThrAlaSerThrProAlaGluPhePro 170
                                                                                                                                                                                                                                                                                                         ValProThrGlyThrGlyGlyGlyValProThrGlyThrGlySerPheThrValThrGly 159
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214638. .217165
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220987. .222215
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and orf3 genes, complete complete
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NFIIIIAYEFSPIKVESYNILTVSPTKFLLTINISSSVGINAVQFLSTVSKSSYEFLI /translation="mfcTsfsnnffkyTsylyQfdTnsvvkGfpyGfsGdnnnyknnI CfERTPQATYINfRTENNYDDYKTFNVPELRRKLTKKKKKKLLKSKYYFfLNINfIN

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AUTHORS
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A shared internal threonine-glutamic acid-threonine-proline repeat
defines a family of Dictyostellum discoideum spore germination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-FEB-1995) Herbert L. Ennis, Roche Institute of Molecular Biology, 340 Kingsland Street, Nutley, NJ 07110, U. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 29 (31), 91002566
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                                                                                                                             LKNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEYSTLFLKVTGENVNEIDFTIINQNGHNPLVKTNFTIEYNKFF FPNLSAVPUNLEVESDMFCTSFSNNFFKYTSVLYGFDTMSVVKGFFYGFSGDNNNYKN NICFERTPQATYINFTENNYDDYKTFNVFELRFKLTKKKKKKLLKSKYYFFLNINFINNFIIIIAYEFSPIKVESYNLLTVSPYKFLLTINISSSVGINAVQFLSFVSKSSYEF INNFIIIIAYEFSPIKVESYNLTVSPYKFLLTINISSSVGINAVQFLSFVSKSSYEFLLTSGKYNGTYQAVIDVYNTPSFRDENGNWLRLYDGSIVSSDPIVYFKLPSIPSMYKI
                                                                                                                       MSCKGDHLVCK&NYLTCKVNISEGTPFHVHDSSLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(448. .1081,1189. .3926)
/note="orf1; similar to CelA, encoded by GenBank Accession
Number M33861, and CelB, encoded by GenBank Accession
Number M33862; contains TETP repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313. .391
/protein_id="AAB54081.1"
/db_xref="GI:2081631"
                                  /evidence=not_experimental
/product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="unknown"
                                                                    codon_start=1
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/db_xref="GI:2081632"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="Ax3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="270G3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .4675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _type="amoeba"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .312,392. .1110)
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BASE COUNT 1709 (
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                                                                                                                      RESULT 26
AC116957_0
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Best Local Similarity:
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Sequence split in
Fragment Name
AC116957_0
AC116957_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ProThrAlaGluProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAACTGAAACTCCAACTCAAACACCAACTCAAACACCAACTGAAACTCCAACCCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProIleAspIleProProValAspThrThrAlaAlaProGluProSerGluThrAlaGlu 108
                                                                                                                                                                                  CCAACACCAACACCAAACCCAGGT---AATTGTAATGTTAGTGTT 2927
                                                                                                                                                                                                                   ProAlaGluPheProGlyAlaGlySerAsnValArgAlaSerVal 180
                                                                                                                                                                                                                                                            CCAACTGAAACTCCAACTCCAACTCCAACTGAAACTCCAACCCCAAACCCCAACACAAACA
                                                                                                                                                                                                                                                                                              ProThrGlyThrGlySerPheThrValThrGlyArgProThr-----AlaSerThr
                                                                                                                                                                                                                                                                                                                                     CCAACTGAAACTCCAACTGAAACTCCAACTGAAACTCCAACTCAAACTCCAACTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                   CCAACTGAAACTCCAACTGAAACTCCAACTGAAACTCCAACTGAAACTCCAACTGAAACT 2769
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746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTRDQDFYNIAYLENDEIPRDLPFSLISLDPVTYSYLTSVRLIN
NIMYPFTFDPTINKFTSKFVIPANTAFDKISFAIIGGLSTEFYYSGFTINNSPAFDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGDKYNGTYQAVIDVYNTPSFRDENGNWLRLYDGSIVSSDPIVYFKLPSIPSMYKILK
NL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="unknown"
/protein_id="AAB54080.1"
/db_xref="GI:676859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFMSCKGDHLVCKSNYLTCKVNISEGTPFHVHDSSLQ"
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45.26%
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AUTHORS
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AUTHORS
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SOURCE
ORGANISM
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VERSION
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1 (bases 1 to 405682)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K., Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum chromosome
AX4, Complete sequence.
AC116957 AC116962
AC116957.2 GI:28829949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany on or before Mar 4, 2003 this sequence version replaced gi:20066269, gi:19920061, gi:19919989.

CDS predictions from GeneID do not necessarily reflect true generative Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-MAR-2003) Genome Analysis, Institute of Biotechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 405682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
intrp://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biotechnology, Beutenberstr.
3 (bases 1 to 405682)
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Baumgart,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deutsche Forschungsgemeinschaft (DFG) Location/Qualifiers
                                                                                                                /translation="mmaktkgsyevfhytvtkdkvnkglcdiaryfvpeyrnskdedl
tiqklinggitnvltylvedknieokyryllpvvirlygykseeiidrkneligtgadon
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mptikkmaalapdvypvpekneyyosinvkknieegknleorlaqliseivfchindll
sgniiydpsqncasfidfeyanynfrglelgnhfneyagfgddyslydnkesqihflt
dyhrslfkteptodeleklyiesnofslashlymgfmaivQamnsqidfdyleygkar
                                                                                                                                                                                                                                 /map="1685067-2090751"
complement (join (644. 776,858. .1605,1712. .1880))
/note="GeneID exon scores (in order of location ranges):
10.65, 75.03, 18.74 - GSCJ_ID dd_03093"
/codon_start=1
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/protein_id="AAO52440.1"
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/codon_start=1
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                                      133.16, 0.23 -
                                                           join(3721. .5364,54
/note="GeneID exon
                                                                                                FDRYYETRDQFLNLN"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:44689"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Dictyostelium
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .405682
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405682 bp
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GSCJ_ID dd_03097"
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1, Jena 07745, Germar
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                                                           location ranges):
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Query

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Sg

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/codon_start=1
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/product="hypothetical protein"
/protein | d="nAo52443.1"
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/db_xref="G1:28829953"
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(YNNNLKRRTLLNY KNYKLIIEDNNGEIGFTPLTNRRYPLPYGVERVEVDCSSITIG
DHWIPDTCKSIYFNNFNQQKLNRNIISNSLTTIFFGNSFNQPLSDSNGLPMLPKKLKT
LSLGQSFQQTIQRNELPQSLTELFLDSSFYGGIILNESIFKSIFTSHYEFFTIRKNHFD
TKSISKGTVSLKIGCYFRNQTIKANHFDINTSLEIDNISKIEIEPNSLFLSIKTLRIG
SIELDSDNILPPNIKKLSIYGDYHSCFLPKSIESLKITSFFNLSKISFNNFRNLTSSK
IEKLSDSVLEEGVFFNTLLRIVLSCPRIKKLSNGIFPNSLKKLKEFNHFIANGDLPS
LEKLSDSVLEEGVFFNTLLRIVLSCPRIKKLSNGIFPNSLKKLKEFNHFIANGDLPS
ILFHLRIYNINHHSI"

Join(13144. .14052,15655. .15768)

note="GeneID exon scores (in order of location ranges):

36.56, 7.78 - GSCU_ID dd_00940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="mdniiysylinnynnknneeqeeeekkhlndlkglndqofqtln
NHIQNLKNTFTTNNSNDEVIYNHSITDNNNNSNDTINNRNKRIAFDCSILIIIKNNLN
HHITIKNNDNSNNLNGLILKPQPDLNNKIRTNQQIDQTIDNNYKLFKKVWGNIFIRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSSGSGSNSPELSTNSSSTNSNNSVTNIKK"
join(1002. 10168,10786. 12082)
/note="GeneID exon scores (in order of location ranges):
0.26, 60.31 - GSCJ_ID dd_00942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKKGSGNGNGGVTSDQDDEEEDEEEDDEEEEEEEDDDEINEDEEISATGTMVVRKKK
NKSTKKSNKKKKKKNIJSTIGKSGSGNNLLHVAPNKPLPITPPFSISMTNEFKQLETK
LFTYIDSSNQKIVNDIKNEIKQLESSIIKIININQQQQSPILLALEEIKQNOHTTSQ
PKQMGKLSATMLNEKKLISSEPPSSNSPLTNSVNSSLTTTTTTTTFVLSRQSFFSS
GSISSSSFLRNSAIMSAVNNSSTTTTNSNSSSSNGGGSGVDISPTNTGRASPSIM
KRFTTSSSSSFLSSSSBGFAFNSNSNSSSSDLKRHVITPEELNNSNLVKNKVKMFEDD
                                                                                                                                                                                                                                                                                                                                                                                                                               SIEVLKLPNYDYPIKNGDLPSSLNVLKLQDHCISTIQRDALPPNLKLFYFHGRELRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSNLKLSNNNNGNQKESSSFFQKVMKSPSTQNLLNSFSSNNSNN
NLSNSGSNEVKDTTTNSPSQLPPNYTPPPPPHQIRNSSSIEGGEFSLLNNENSDNNNN
NNNNNNNNNNNNNNNNNNNHOLARTESSVSIISSSSGSNSGQPNLQRHSSNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mold). Kinase responsive
/protein_id="AAO52442.1"
/db_xref="GI:28829952"
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NNEYDINNI DKNYNKENS I ERLEFLKKLI INNHENSENSEIRRLITGOHIKKYDSLSD
ENWLYGYI YNLFKNEFLSKODTWSLNI ODFKGI FKLKPSSI RRLITGOHIKKYDSLSD
ENWLYGYI YNLFKNEFLSKODTWSLNI ODFKGI FKLKPSSI RRLITOOHIKKYDSLSD
KYQNLINNNNNNNNNNNNNNNNN I GNAI INNI I KDDEGTLNEKI I LKYKKSTTKVSTP
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NEQLYQVTGELWFKLLDKFSQDFEGSSSTTSSSSSTTSTFGIRUKPPPFITLSICYLA
CVYLREPVIISDFISLAQGKIASFTWETTWEFSWSNSNSTFINFARISDDICKYLD
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                                                                                                                                                                                                                                                                                                                                                                                                              PNLIWPTSFEFAYISEASFNFINSIDLDFFTNHIRLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKRIG
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                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="similar to Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/db_xref="GI:28829951"
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US-10-081-935-4 (1-194) x AC116957_0 (1-110000)
                                                                                                                                                                    ACAGGTAAAGGATTTAAATCAGTTACTGGTGCAACATTCAATTATAAATCAACTACTAAA 48919
                                                                                                                                                                                                                                                                    GATGITCCAGITATTACAGGITCTGATAGAATTTCTACATTAGGIGGIGATTTATGGITA 48859
                                                                                                                                                                                                                                                                                                               AspIleProProCysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAsp-----
                                                                     CCATTACAAGTTAAAAAAACTGTTGGGGGGTGCTGCTATTTTATTAGGCGGTATCTCTGAA 48979
                                                                                                                   ProGlyGlnIleThrProCysValGluGluAlaCysProLeu-------
                                                                                                                                                                                                                ------GlyCysThrArgLeuThrAspPheLysCysHisCysSerLysProGluLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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NSNDETIYTHSITDNNNNDTIDNRNKRIAFDCSILIIIKNNLNHHITINNKNINKNINNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
join(2I335. .21528,21616. .21928)
/note="GeneID exon scores (in orc
-5.52, 10.92 - GSCU_ID dd_00435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(18782. .18911,19094. .20841)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRCSDIILVDHWIPDTCKSIIFSHFNQQLTRNIIGNSLTSIDFGKDFNQSLSDKNGIPWLPRTLKSLTFGKSFQHSIHRDEIPPSLTSLILDPKYKGVLEYGSIRKVTTLHYYFDSKGAKLDSTSIPGGTTSLEFDSFFDQTIEKGMISHNVTSLKFFFCNSIIKSLLFSIIKTLHYSDXFDXITALSVYTFSDIKILPKTIQKLKIMDFSPRSQLDHSIIKTLPKTIQKLKIMDFSPRSQLDHHSFYFLKNLTSLNFDAKQVDLTNVKFPNIISRLTLAVSDYLEFNDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (22154. .22339)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="GeneID exon scores (in order of location ranges):
0.40 - GSCU_ID dd_00433"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNLSIVTFSDIGILPKTIEKLKIIGSNNFTQLDSHSFHIFENLKSLELNAIGVDLTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(15826. .16011,16072. .17106)
/note="GeneID exon scores (in ord
/not31.02 - GSCU_ID dd_00422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQNNFKKLKLFNFNQPLNVGDLPSSIEGCPAVRAIRANGLIQALLSDHGLDVNNLNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AA052445.:
/db_xref="GI:28829955"
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D exon scores (in order
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Matches:
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AC119773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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Allen, C., Allen, H., Alsbrocks, S., Amin, A., Angulano, C., Allen, H., Alsbrocks, S., Amin, A., Angulano, D., Alvel, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barbatead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Dederich, D., Davils, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Duhn, H., Divya, K., Delgan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Fosteer, M., Foster, P., Fraser, C., Mamilton, C., Hamilton, C., Hamilton, K., Gerrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haadand, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hadeun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulwyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Liu, J., Liu, J., Liu, J., Liu, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48980 ATGGATCAAGGTAGTAACTTTAGTATTATATTAGAAAATGATAAATCAATATCTTCAAAT 49039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49160 ACACCAÁCTCAAACACCAÁCTCAAACTCCAÁCTGAAACACCAÁCTCAAACTCCAÁCTGAÁ
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Rattus norvegicus clone CH230-150P22, ***
***, 7 unordered pieces.
AC119773
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AC119773.6 GI:25095179
HTG; HTGS_PHASE1; HTGS_I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RATTUS norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluProThrAlaValProThrGlyThrGlyGlyGlyValProThrGlyThrGlySerPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACCAACCGAAACACCAACT---GAAACACCAACTGAAACACCA 49321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrvalThrGlyArgProThrAlaSerThrProAlaGluPhePro 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACCAACTCAAACTCCAACTGAAACACCAACCCAAACACCAACCGAAACACCAACTCAA 49279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTCANACACCAACACCAACTGAAACACCAACTGAAACACCAACTCAAACACCAACTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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SEQUENCING IN PROGRESS
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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:22856367.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneet, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 222896)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                               shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 222896)
----- Genome Center
                                                                                                                                                                                                                                                                                                                               and separated
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary, Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will * NOTE: Estimated insert size may differ from sequence length be preserved Center project Information
Center project name: GVPS
Center clone name: CH230-150P22
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202212 bases at least Q40
Consensus quality: 206295 bases at least Q20
Consensus quality: 208887 bases at least Q20
Estimated insert size: 209030; sum-of-contigs estimation 130231 130331 150794 150894 217181 217281 Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Quality coverage: 6x in Q20 bases; sum-of-contigs estimation 130230: contig of 130230 bp in length 130330: gap of unknown length 150793: contig of 20463 bp in length 150893: gap of unknown length 217180: contig of 66287 bp in length 217280: gap of unknown length 218456: contig of 1176 bp in length 218556: gap of unknown length

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                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium 1 (bases 1 to 4284)
Giorda,R., Ohmachi,T., Shaw,D.R. and Ennis,H.L.
A shared internal threonine-glutamic acid-threonine defines a family of Dictyostelium discoideum spore of
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U20661
                           Biochemistry 29
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880 219879: gap of unknown le

980 221385: contig of 1506 by

186 221485: gap of unknown le

186 222896: contig of 1411 by

Location/Qualifiers
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/mol_type="genomic DNA"
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KY11SKERLKMATSKEKEELKFLHNTRGTEQRLRFIDRGDGTLNIRDFYGKSICLKKD
PRFFTNKYYGFYGGSAQDECIFTYILNADGTYNFKNKQNTYLSSDSGEEFFGRKSLGS
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2 (bases 1 Giorda, R.,
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orda,R., Ohmachi,T.,
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1735. .3117
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/note="orf1; similar to CelA, encoded by GenBank Accession Number M33861, and CelB, encoded by GenBank Accession Number M33862; contains TETP repeat"
/codon_start=2
/note="internal repeat protein; putative spore germine specific protein; similar to CelA, encoded by GenBank Accession Number M33861, and CelB, encoded by GenBank Accession Number M33862; contains TETP repeat"
                                                                                                                                                       NYSSNSNDLOPTDSSTTDPPYTDPPITDPPITDPPYTDPPITEPPYTETPKPTINPFF
NTPVPICSQXIDQCLTVLNSQDLEFIDKKGRDQSMVLEYDGNLBQTFSIREKGGMYIC
LSGEHYHFSEKLKGRLNANKDGRDCTFNLITQFNIDKQANLYSFRSPNDQYIQSDETT
RFISTKPGGLGSQSQFFIYFSHSLGPNLD"
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KYTGISKLSHLNSKFKIIYLFLILLFLMTILVNLNRHYQTKFSIIQRNNIFLSITPES
NPIKKPSPTOSSDYNQYSEGSQSSYESSSSSSSSSSSSSSSSSSSSSSSSSI
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/db_xref="GI:2081630"
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                                                                                  germination
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/codon_start=1 /evidence=not_experimental

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                                                                                                                   Rattus norvegicus clone CH230-9E3,
AC095211
AC095211.4 GI:22773101
HTG; HTGS PHACE
                                                                               Rattus norvegicus (Norway rat)
                                                                                                                 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
Muzny, D.Marie.,
                                              Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                Rattus.
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              (bases 1 to 252801)
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/db_xref="d1:684939"
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nnnnedededdldnynnseklmdsmkinselyqiypklsyktikessignknkidkiq
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Abramzon, S.,
                                                                                                                                                                     linear HTG 03-OCT-2002 SEQUENCING IN PROGRESS ***.
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Adams, C., Alder, J
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Allen, C., Allen, H., Alsbrooks, S., Main, A., Anguiano, D.,
Bayalbechi, W., Angaria, D., Barbor, M., Barnets, adden, M., Benshmed, F.,
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Bissalb, M., Bart., Blanch, Blankenburg, M., Byth, P., Boonn, B.,
Crackens, V., Carter, K., Cavazo, I., Ceasar, H., Conter, N., Chen, Y., Y., Martin, K., Martin, X., Martin, X., Martin, X., Martin, Y., Martin, Y
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REFERENCE AUTHORS TITLE

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BASE COUNT
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                            ProThrHisGluProThrGluGluProThrAlaValProThrGlyThrGlyGlyVal
                                                                                                                                                                                                                                                           AlaArgIleSerValSerAsnIleValValAspGlnCysSerLys-----AlaGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLysProGluLeuProGlyGlnIleThrProCysValGluGluAlaCysProLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and the accession number will be preserved.

1 252801: contig of 252801 bp in length.
          -----ProAlaGluPheProGlyAlaGlySerAsnValArg 177
                                                          ProThrGlyThrGlySerPheThrValThrGlyArgProThrAlaSerThr-----
                                                                                                                                                                                                                                                                                                             ProThrAlaGluProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                               ProIleAspIleProProValAspThrThrAlaAlaProGluProSerGluThrAlaGlu 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name:
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251753. .252801
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49651 c 49432 g
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|mol_type="genomic DNA"
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AUTHORS
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18 Van Sluys, M.A., de Oliveira, M.C., Monteiro-Vitorello, C.B., Miyaki, C.Y., Furlan, L.R., Camargo, L.E.A., da Silva, A.C.R., Moon, D.H., Takita, M.A., Lemos, E.G.M., Machado, M.A., Ferro, M.I.T., da Silva, F.R., Goldman, M.H.S., Goldman, G.H., Lemos, M.V.F., Tsai, S.M., Carrer, H., Carraro, D.M., de Oliveira, R.C., El-Dorzy, H., Tsai, S.M., Carrer, H., Carraro, D.M., de Oliveira, R.C., Nunes, L.R., Siqueira, W.J., Coutinho, L.L., Kimura, E.T., Ferro, E.S., Harakava, R., Kuramae, E.E., Marino, C.L., Giglioti, E., Abreu, I.L., Alves, L.M.C., do Amaral, A.M., Baia, S.S., Blanco, S.R., Brito, M.S., Carnavan, F.S., Celestino, A.V., da Cunha, A.F., Fenille, R.C., Ferro, J.A., Formighieri, E.F., Kishi, L.T., Leoni, S.G., Oliveira, A.R., Rosa Jr., V.E., Sassaki, F.T., Sena, J.A.D., de Souza, A.A., Truffi, D., Tsukumo, F., Yanai, G.M., Zaros, L.G., Civerolo, E.L., Simpson, A.J.G., Almeida Jr., N.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-DEC-2001) Instituto de Biociencias, Universidade Sao Paulo, Rua do Matao, 277, Sao Paulo, SP 05508-900, Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paulo, Rua do Matao, 277
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iveira, R.C., Ferro, E.S.,

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FEATURES

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1110. .1508
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97. .1113
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                                                                                                                                                                                                                                                                                                                               _tag="PD0738"
                                                                                                                                                       table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pef1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor"
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Pred. No.:
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                                                                                                                                                                                                                                                     Score:
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252627 GTCTTGAGTGCCTGTGGTGGTGGATTAGTTCGTATAGATACACCTACACCGACACCCCACA 252568
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gene

Sg

gene

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                  US-10-081-935-4 (1-194) x AE012556
79 ValValAspGlnCysSerLysAlaGlyValProIleAspIleProProValAspThrThr 98
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KRQQLSPSDVSKOMGSGTYSTESKVRLAQGREAVLRAVVRMGGGRIPGATYTTLHWEE
GIAWQ"
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2949. .4103
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4084. .4716
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4706. _5473
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located using Blastx/Glimmer"
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                                                                                                                                     48.9
161.50
46.24%
41.94%
15.79%
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                                                        (1-300029)
                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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39
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SOURCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (8230) gene, complete
AF269242
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(Rasmodium falciparum transmission-blocking target antigen Pfs230 gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-MAR-2000) Department of Parasitology, Sun Yat-Sen University of Medical Sciences, 74 Zhongshan Road II, Guangzhou, Guangdong 510089, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shan,Z.X., Yu,X.B., Li,X.R., Ma,C.L., Fang,J.M. and Wu,Z.D. Structure of the gene for Plasmodium falciparum isolate FCC1/HN transmission blocking target antigen, Pfs230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyArgProThrAlaSer---ThrProAlaGluPhePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaValProThrGlyThrGlyGlyGlyValProThrGlyThrGlySerPheThrValThr 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTACACCCACACCCACACCCCACACCCCACACCCCACACCTACACCCCACACCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 9435)
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                             LFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKEIRMRKDTSVKIKQRTCPFHKEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         country="China"
                                                                                                                                                                                                                                                                                                                                                                                                        .9435
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                                                                                                                                                                                                                                                                                                                                       target antigen Pfs230"
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Alignment Scores: 2.14 Length: 9435
Pred. No.: 161.00 Matches: 35
Score: 162.00 Matches: 15
Percent Similarity: 48.54% Conservative: 15
Best Local Similarity: 33.98% Mismatches: 37
Ouery Match: 15.74% Indels: 16
DB: 3 Gaps: 3
US-10-081-935-4 (1-194) x AF269242 (1-9435)

BASE COUNT ORIGIN

밁 Ś 밁 Ś 밁 S 5 밁 문 S 1382 GGATATATTTCACCTTGC------1352 TCTACATAT---77 57 PheThrVal 157 CCTACCTCTTCACCTACCTCTTCACCTACCTCTTCATCTGCATCTTCATCTTCA ProThrAlaValProThrGly-----ThrGlyGlyGlyValProThrGlyThrGlySer 154 CCTACCTCTTCACCTACCTCTCACCTACCTCTTCACCTCTCACCTTCACCTACCTCTTCA 1185 ProThrAlaGluProThrAlaGluProThrAlaGluProThrHisGluProThrGluGlu 136 AsnIleValValAspGlnCysSerLysAlaGlyValProIleAspIleProProValAsp 96 GlyGlnIleThrProCysValGluGluAlaCysProLeuAspAlaArgIleSerValSer 76 TCACCTTCTTCTTCACCTACCTCTTCACCTTCTTCTTCA 1305 ----CTTTCTTTTCA

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Cardenas, V., Carter, K., Chen, G., Chen, R., Chen, Y., Chen, C., Coyle, M., Cree, A., D'Souza, L., Davia, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davia, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagy, N., Forbes, L., Foster, M., Garca, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Ghaisi, A., Ganta, R., Garcia, A., Garner, T., Garcaxa, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gharathe, P., Haaland, W., Hanilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hulyk, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kaff, C.L., Lebow, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Warrin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin
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AC109525 GI:23603814
HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Norway rat)
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Mammalia; Eutheria;
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SEQUENCING IN PROGRESS
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On Oct 9, 2002 this sequence version replaced gi:22795167.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of S contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved
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235124
246066
246166
474602
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475762
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Consensus quality: 380245 bases at least Q40
Consensus quality: 385911 bases at least Q30
Consensus quality: 385971 bases at least Q30
Consensus quality: 389797 bases at least Q30
Estimated insert size: 390792; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GPHZ
Center clone name: CH230-255D23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
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Center: Baylor College of Medicine
/note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                /clone="CH230-255D23"
                                                                                                                                                                                   organism="Rattus norvegicus"
                                                                                                                                db_xref="taxon:10116"
                                                                                                                                                                                                                                                                       235023: contig of 235023 bp in length
235123: gap of unknown length
246065: contig of 10942 bp in length
246165: gap of unknown length
474601: contig of 228436 bp in length
474701: gap of unknown length
475761: contig of 1060 bp in length
475861: gap of unknown length
478861: gap of unknown length
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Muzny, D. Marie, Metzker, M.Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Avyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blaiwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blyvant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claeveland, C., Cokrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
                                                                                                                                                                                                                                             Rattus.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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350281. .351366
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358886. .361234
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287702. .289205
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84236 c 86247 g 111645 t 85141 others
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406035. .407045
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TITLE JOURNAL

COMMENT

Web site: http:/

Center:

Baylor

of Medicine

 Genome Center College

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Egan, A., Buscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C. Evans, C.A., Falls, T., Fan, G., Franger, C.M., Gabisi, A., Ganta, R., Garcia, A., Garcar, M., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Harlen, P., Haaland, M., Hamilton, C., Hamilton, K., Harlon, R., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hluyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Loulseged, H., Lozado, R.J., Lopez, J., Liu, J., Lorenshawa, L., Lolseged, H., Lozado, R.J., Lu, X., Ma, J., Mahreibawai, M., Mahrintartne, M., Mahroud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavijevis, C., Miner, G., Minja, E., Montemayov, J., Moore, S., Morenshayevis, C., Neal, D., Newton, N., Nguyen, N., Nurphy, M., Nair, L., Pasterriak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Ph., L. L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Ph., L. L., Plopper, F., Roindexter, A., Popovic, D., Primus, E., Ph., L. L., Planker, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shen, H., Stein, C., Shatsman, S., Shen, H., Shety, J., Song, X.-Z., Sorelle, R., Sosa, J., Stein, R., Wallson, R., Walson, R., Walton, L., Walter, B., Wang, J., Walter, B., Wang, J., Walter, R., Satth, D.R., Holt, R.A., Smith, H.O., Walter, R., Satth, H.O., Walte
AL Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:22772430.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237019)
Rat Genome Sequencing Consortium.
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Egan,A., Escotto,M.
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ACCESSION
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AP000721/c
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ORIGIN
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sequence.
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                                         Homo sapiens
                                                         AP000721
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                               GlyGlyValProThrGlyThrGlySerPheThrValThrGlyArgProThr------
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                                                                                                                                                                                                                                                                                               ThrAlaGluProThrAlaGluProThrGluGluProThrAlaGluProThrAlaGluPro 125
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                                                                                                                                        AlaSerThrProAlaGluPhePro
                                                                                                                                                                                                                          Assembly program: Atlas; Consensus quality: 229894 bases at least Q40 Consensus quality: 231178 bases at least Q30 Consensus quality: 231607 bases at least Q20 Estimated insert size: 244941; sum-of-contigs estimation quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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228959. .231233
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227374. . 228903
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              Rattus norvegicus clone
AC106943
AC106943.4 GI:22857065
HTG; HTGS_PHASE2; HTGS_E
 Rattus norvegicus
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             HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
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US-10-081-935-4 (1-194) x AP000721 (1-124636)
                                                                                                                                                                                                                 52059 CCAGCCAACACCCCGGCCAACAC-CCTGGTGTGGGTAGTGGCGTGGAGTTCCTGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-NOV 1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170 on Jan 31, 2003 this sequence version replaced gi:21623945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 124636)
Hattori,M., Ishii,K., Toyoda,A.,
Fujiyama,A., Yada,T., Totoki,Y.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               ProThrAlaGluProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAATATGCCAACCAACACCCCAGCCAACACACCCAACACCCCAGGCAACACTTCAA 52236
                                                                                                                                                                                                                                                          ---AlaSerThrProAlaGluPheProGlyAlaGlySerAsnValArgAlaSerValGly 181
                                                                                                                                                                                                                                                                                                                                                                                                               CCAACACCCTGGGCAACACCCCAGCCAACACCCCAGCCAACACCCCAACCAACA---ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAACACCCCAACCAACCCCAACCAACACCCCAGCCAACCCCCAACCAACACCCCAA 52176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProlleAspIleProProValAspThrThrAlaAlaProGluProSerGluThrAlaGlu 108
                                                                                                                                                                                                                                                                                                                                                            GlyGlyGlyValProThrGlyThrGlySerPheThrValThrGlyArgProThr----- 162
                                                                                                               Pro-----ThrHisGluProThrGluGluProThrAlaValProThrGlyThr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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259772 bp
clone CH230-36G6,
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Watanabe,H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, Q., Wangs, S., Warren, J., Warren, M., Wei, X., White, F., Wang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., Yoon, V., Waisht, D., Zhou, X., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 14, 2002 this sequence version replaced gi:21737094. On Sep 14, this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259772)
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Direct Submission
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Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
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                    feature table below
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124 GluProThrAlaGluProThrHisGluProThrGluGluProThrAlaValProThrGly 143
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COMMENT

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US-10-081-935-4 (1-194) x AC106943 (1-259772)
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently

consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                        Similarity:
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                                      SerGluThrAlaGluProThrAlaGluProThrGluGluProThrAlaGluProThrAla 123
CCGCCCACGCCACGCCACGCCACGCCACGCCACGGCACCGCCACGCCACGCCA
                                                                                                                                                                             SerLysAlaGlyValProlleAspIleProProValAspThrThrAlaAlaProGluPro 103
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Consensus quality: 233717 bases at least Q40
Consensus quality: 233717 bases at least Q30
Consensus quality: 236729 bases at least Q30
Consensus quality: 236822 bases at least Q20
Estimated insert size: 252037; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-36G6
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plasmodium falciparum
plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 9636)
williamson, K.C., Criscio, M.D. and Kaslow, D.C.
Cloning and expression of the gene for Plasmodium falciparum
transmission-blocking target antigen, Pfs230
Mol. Bicchem. Parasitol. 58 (2), 355-358 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Plasmodium NF54) gametocyte cDNA to mRNA.
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TYKNHKDVKYPEQSSVLSPLSSADSLGKILNFLDTQETVCLTEKIRYLMLSINELGSD
NNTFSVTFQVPYIDIKEGFFYFMFGCNNNKGEGNIGIVELLISKQEEKIKQCHFHSSK
LDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYLQPENCFNNV
YKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKXIKV
IITKNDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFN
                                                                                                                                                                                                                                                                                                                                    TESGDTAVSEDSYDKYASNN'INKEYVCDFTDOLKPTESGPKVKKCEVKVNEFLIKVKI
I CPLKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISFTVNEKENN
FKEGVIEFTLEPVVHKATVEYFICDNSKTEDDNKKGNRGIVEYVVEPKUKINCCAFL
DEDEEEKYGNOIEDDEHNEKIKMKTFFTONIYKKNNIY PCYMKLYSGDIGGILFPKN
IKSTTCFEBMIPYNKEIKMKLKENKSLGNLYNNSVYNKEMAKYFNYQYVHIPFSYKD
TLNLFCSIILKEESNLISTSYLVVSINEELMFSLEPDYESFVPIKKTIQVAQKVN
NKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIF
                                               NINGILYLKNNLANFTYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKV
LRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGKKKPADTDAN
                                                                                                 YIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLI
LYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKV
KGCSFDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLT
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LFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKEIRMRKDTSVKIKQRTCPFHKEG
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/product="Pfs230"
/protein_id="AAA29734.1"
/db_xref="GI:294176"
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KDIEQYVLQVNLKAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHC
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RESULT 37

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Best Local Similarity:
                                                        AR178096/c
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AKI78096 9636 bp
Sequence 1 from patent US 6316000.
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                                                                                                                                                                 ValThrGlyArgProThrAlaSerThrProAlaGluPhe 169
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                                                                                                                                                                                                                                 CCTACCTCTTCACCTACCTCTTCA
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LKDQDDRLSRHDDYNKNHTY ILYDSNEH I CDY EKNESLI STLPNDTYKIQKSI CKI NA
KALDVVT I KCPHTKNFT PKDYFPNSSLI ITNDKKI VI TFDKKNFVTY I DPTKKTFSLKD
IYIQSFYGVSLDHLNQI KKI HEEMDDVHLFY PPHNVLHNVLUNHI VNLSSALEGVLF
MKSKVTGDETATKNTTLPTDGVSSILI PPYVKEDI TFHLFCGKSTTKKPNKKNTSLA
LIHIH I SSNRNI I HGCDFLYLENQTNDA I SNNNINS I FTHKWTENNLI CDI SLI P
KTVIGI KCPNKKLNPOTCFDEVYYKQEDVPSKTI TADKYYTFSKDKIGNILKNA I SI
KNPDEKUNTYTVLI LPEKFEEELI DTKKVLACTCDNKY I I HMK I EKSTMDK I KI DEKK
TIGKDJ CKYDYTTKATCELI DTI DSSVLKEHHTVHY SI TLSRMDKLI I KYPTNEKTH
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LPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNEANKVKKLFDLSTKVEL
DHIKONTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPOSRAII
KYYDLODKNFAKYLRKL"
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DPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKPLDYINKLLFSCS
CKTSHTNTIGTMKVTLNKDEKEEDDFKTAQGIKHNVHLCNFFDNPELTFDNNKILC
KIDAELFSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNE
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LIYIFVRKAVSENSFKLCDFTTGSTSJMELNSQVKEKKCTVKIKKGDIFGLKCPKGFA
JFPOACFSNYLLEYYKSDYEDSEH NYYIHKKKYNLKFKDVIELMDENFRELONIOQ
YTGISNITDVLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVY
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PGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGII
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/rpt_type=direct
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                                                                  1 (bases 1 to 9636)
Williamson,K.C. and Kaslow,D.C.
Cloning and expression of Plasmodium
blocking target antigen, Pfs230
Patent: US 5733772-A 1 31-MAR-1998;
                                                                                                                                                              Sequence 1 from patent 195887 195887.1 GI:3940357
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Williamson,K.C. and Kaslow,D.C.
Cloning and expression of plasmodium falciparum transmission-blocking target antigen, PFS230
Patent: US 6316000-A 1 13-NOV-2001;
Location/Qualifiers
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: US 5733772.
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                                                                                                                                                                                                                                          Unpublished (1993)
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                                 /gene="8230"
179. .9586
                        /gene="8230"
                                                                                                                                                                                                                                                                                                                                               GI:605630
                                                              'gene="8230"
                                                                                   /gene="8230"
                                                                                                                                     clone="8Y"
                                                                                                                                                                   /strain="3D7"
                                                                                                       germline
                                                                           .9654
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158.00
46.02%
30.97%
15.44%
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1485 TCTACATAT-----TCACCTTCTTCTTCACCTACCTCTCACCTTCTTCTTCA 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 9654)
1 (bases 1 to 9654)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnIleValValAspGlnCysSerLysAlaGlyValProIleAspIleProProValAsp
                                                                                                                                                                                                                                     /dev_stage="sexual asexual stages"
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                                                                                                                                                                                                                                                                                                 /db_xref="taxon:36329"
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                                                                                                                                                                                                                                                                                               /map="chromosome
                                                                                                                                                                                                                                                                                                                                                                         organism="Plasmodium
                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
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Percent Similarity: Best Local Similarity: BASE COUNT US-10-081-935-4 (1-194) Pred. No.: Alignment Scores: 1545 57 GGATATATTTCACCTTGC--GlyGlnIleThrProCysValGluGluAlaCysProLeuAspAlaArgIleSerValSer 76 9587. .9654 /gene="s230" a 976 c 1 /translation="MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFH LFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKEIRMRKDTSVKIKQRTCPFHKEG SSFEMGSKNITCFYPIYGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN DEKCHHETYSKDNKTVKKFREVIPNIDIFSLHNSNKKVAYAKVPLDYINKLLFSCS
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KIDAELFSEUTIQLPIFGTKIVLESEDFKTAGGIKHNVHLCONFEDDFLITEDNINKIVLC
KIDAELFSEUTIQLPIFGTKIVLESEQQNEEYKKFSLKPSLVFDDNINDIXVIGKENE
VSISLALKGVYGNRIFTEDKNGKKGEGISFTIPPIKQDTDLKFIINETIDNSNIKQR
LIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKGDIFGLKCPKGFA
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YTGISNITDVLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVY
CTMQVESDNRNFDNIKKHENVIKDFLLFNIEKYALLDDEEKGKIKQQQEEEGQQQI
LKRODDRLSRHBDYNKHHTYILYDSNEHHICVYKEKNESLISTLPNDTKKIGKSICKIN
KABLDVUTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKO LYNEEKVÜLLHFYVFLPÏYIKDIYEFNIVCDNSKTMMKNQLGGKVIYHITVSKREQKV
KGCSFDNEHAHMFSYNKTNVKKCIIDAKPKDLIGFVCFSGTILKINCFKDAIVHTNLT
NINGILYLKONLANFTYKHQFNYMEIPALMDDISFKCICVDLKKKKYNVKSPLGPKV
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PESIIESLSINESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLEL
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YALLKPLDTLYVKCPTSKDNYEAAKVNISHOEDSILESILEKFHNFETLESKKP
GNGDVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVLNEYDDTEEEKDLESIL
PGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGII
HDISNSNRKINGCDFSTNNSSILTSSVKLVNGETKNCEININNKWEVFGIICDNETNL
HIDISNSNRKINGCDFSTNNSSILTSSVKLVNGETKNCEININNKWEVFGIICDNETNL IYIQSFYGVSLDHLNQIKKIHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLF MKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTKKPNKKNTSLA LIHIHISSURNIIHGCDFLYLENQTNDAISNNNNNSYSIFTKNKTENNLICDISIF KTVICIKCPNKKLNPOTCFDEVYYVKQEDVPSKTITADKYNTESKDKIGNILKWAISI NNPDEKDNTYTYLILPEKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKK TIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYPTNEKTH KTLKDKKEVLKLDLDIQYQMFSKFFKRITQNAKYLNI.YPYLIF PPRHHIGKKELKNNP
TYKNHRÜDYKY TEQSS VLSPLSSADSLGKLLNFLDTQSTYCLTEKIRYLNLS INELGSD
NNTTSVTFQVPPYIDI KEPFYEMFGCINNKGEGNIGI VELLISKQEKHEKKEK
LDYFNENISSDTHECTLHAYENDI IGFNCLETTHPNEVEVEVEDAEIYLQPENGFNNV
YGLAKSOLTITILKNAQTYNINNKKTFTFLKIPPYNLLEDSLGCTIKQVVKKIKV
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YGLAKSOLTIKIN YKOLHENFINPRVNKTFDENVEYTCNIKILNFFN
YGLAKSOLTIKOLTYNIONKKTFTFLKIPPOFKKFNNEELHKLIPNSEMLHKTREMLI DEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKN IKSTTCFEEMIPYNKEIKMKENKSLGNIVNNSVVYNKEMNAKYFNVQYVHIETSYKN TLNIFCSIILKEEESNILSTSYLVYVSINEELMHSLFDPYESFVPIKKTIQVAQKVN NKEHDYTCDFTDKLDKTVFSTANGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFP TESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESGPKVKKCEVKVNEPLIKVKI ICPLKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENN FKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRGIVEVYVEPYGNKINGCAFL KYVDLQDKNFAKYLRKL" IHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKP LPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNEANKVKKLFDLSTKVEL DHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAII FENF FVNP FNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKD I DKENKND I QNVEEK I QRDTYENKDYESDDTL I EWFDDNTNEENFLLTFLKRCLMK I F 3.27 158.00 46.02% 30.97% 15.44% × PFAS230A 1432 (1-9654)Length:
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Conservative:
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Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T., James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Angiuoli, S., Petrea, M., Allen, J., Selengut, J., Haft, D., Fraunholz, M.J., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Barrell, B.
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1 (bases 1 to 15148)

Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayron, R., White, O., Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L. Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                  Direct Submission Submitted (02-OCT-2002) The Institute for Genomic Research, Submitted (02-OCT-2002) The Institute for Genomic Research, Submitted (02-OCT-2002) The Institute for Genomic Research, Submitted (02-OCT-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence.
AE001393 AE001362
AE001393.1 GI:384
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Nature 419, 498-511 (2002)
3__(bases 1 to 15148)
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Plasmodium falciparum 3D7
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Location/Qualifiers
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DHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLESIL
PGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGII
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YALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQVISLIEKRFHNFETLESKKP
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Search completed: December 6, 2003, 03:09:16 Job time : 2869 secs
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                                  157 ValThrGlyArgProThrAlaSerThrProAlaGluPhe 169
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Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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equence 10081,	quence 1	equence 6421,	equence 16386,	equence 8, App	equence 9931,	equence 7, App	equence 3703,	equence 19, Ap	equence 16275,	equence 2891,	equence 132, F	equence 3, Apr	equence 1, App	equence 18, Ap	equence 9057,	equence 9220,	equence 15656,	equence 1918,	equence 3, Apr	e 8728,	equence 15674,	equence 15702,	equence 9137,	quence 33, Ar	equence 1, App	quence 1, App	equence 1, App	equence 1, App	equence 20, Ap	quence 20, App	equence 18, App	equence 1, App

ALIGNMENTS

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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                Alignment Scores:
US-10-081-935-2 (1-18) x US-09-103-840A-2 (1-4403765)
                                                                                                                 Score:
                                                                                                                                Pred. No.:
                                                                                                                                                                                  US-09-103-840A-2
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US-09-103-840A-2
                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                 LENGTH: 4403765
                                                                                                                                                                                                  CDC 1551
"n" bases
represent
                                      1.85e+05
47.00
92.86%
64.29%
57.32%
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                                                   Conservative: Mismatches: Indels:
                                                                                                         Length:
Matches:
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US-08-525-697-3
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Best Local Similarity:
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
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SOFTWARE: PatentIn Ver. 2.1
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APPLICATION NUMBER: US/08/525,697
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4004.204
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
SOFTMARE: PatentIn PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: No. 57957640 No. 5795764disk of No. 5795764th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Heldt-Hansen, Hans P
APPLICANT: Dalboege, Henrik
TITLE OF INVENTION: AN ENZYME EXHIBITING MANNANASE ACTIVITY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Christgau, Stephan
APPLICANT: Andersen, Lene N
APPLICANT: Kauppinen, Sakari
APPLICANT: Heldt-Hansen, Hans P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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CITY: New York
STATE: New York
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64.29%
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     4004.204-US
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Best Local Similarity:
Query Match:
                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/525,697
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4004.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0486/9
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                             TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
PRIOR APPLICATION UNMBER: DK 0486
APPLICATION NUMBER: DK 0486
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: //
APPLICANT: //
APPLICANT: //
APPLICANT: //
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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CITY: New York
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TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS:
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                   nucleic acid
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NVENTION: AN ENZYME EXHIBITING MANNANASE ACTIVITY
SEQUENCES: 15
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Heldt-Hansen, Hans P
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Indels:
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GENERAL INFORMATION:

APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David

TITLE OF INVENTION: Genes in the No. 6103886-Recombining if
TITLE OF INVENTION: The Y Chromosome
FILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER APPLICATION NUMBER: 60/041,877
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                            RESULT 6
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Best Local Similarity:
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US-09-058-489-34
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US-08-525-697-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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; LENGTH: 10091
; TYPE: DNA
; ORGANISM: Human
                                                                                                                                                                                                                           Sequence 8612, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/09058489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6103886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 91
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No.:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                         3483 CTTCAACAAATCATGCTTTAGTTACTTTGGTAGCAGAAACCTTGCAACC 3533
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                                                                                                                                                                                                                                                                                                                                                                   ATGAAGCTTTCTCACATGCTCCTCAGCCTCGCCAGCCTGGGGGTGGCGACGGCT 114
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Matches:
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US-08-389-564B-21/c
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 959
LENGTH: 504
TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                         Sequence 21, Application US/08389564B Patent No. 5989870 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8612
LENGTH: 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus
                                                                                 APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: A METHOD FOR CLONING
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
               STREET: 1100 New CITY: Washington STATE: D.C.
COUNTRY:
                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                         134 CAATTTTCACATTCTCTTCTACGTCTAATCGCA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 ATGAAATTCACGCATTCGATCGCGGCCATCGTTGGCGCCGCCACTGGTCACC 120
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U.S.A.
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Matches:
Conservative:
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Indels:
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION NUMBER: GB 86 10600
FILING DATE: 30-APR-1986
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1716.008000G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
                                                                                                                                                                      APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Ilm n, Marja H.
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: A METHOD FOR CLONING ACTIVE PROMOTERS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/932,485
FILING DATE: 19-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                   STREET: 1100 New CITY: Washington
                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
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                                                                  20005
                                                                                                      D.C.
                                                                                                                                               E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
                                                                                     U.S.A.
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Matches:
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RESULT 10
US-08-466-047B-21/c
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6011147
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/932,485
FILING DATE: 19-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 2
                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: Fungal Promoters Active In
TITLE OF INVENTION: Of Glucose
                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
STREET: 1100 New Yorl
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both MOLECULE TYPE: cf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE: 30-AFF.
FILING DATE: 30-AFF.
ATTORNEY/AGENT INFORMATION:
REED, GRANT E.
TOTAL:
41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 41,264
REFERENCE/COCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                      D.C.
                                                                                                                                                                   E: Sterne, Kessler, G
1100 New York Avenue,
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                                                                                                                  U.S.A.
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   Patentin Release #1.0,
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42.00
84.62%
53.85%
51.22%
                                                                                                                                                                       Kessler, Goldstein & Fox P.L.L.C ork Avenue, Suite 600
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Indels:
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Conservative:
   Version
                                                                                                                                                                                                                                                                    The Presence
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/466,047B

SOFTWARE:

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                              APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n. Marja H.
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: Fungal Promoters Active In The Presence
TITLE OF INVENTION: Of Glucose
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 86 10600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41.264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/389,564
FILING DATE: 16-FEB-1995
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TELECOMMUNICATION INFORMATION:
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                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                             STREET:
                                                                                                          COUNTRY:
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                                                                                                                           D.C.
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                                                                                                                                                             IE: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                      Nakari, Tiina H.
Onnela, Maija-Leena
Ilm n, Marja H.
                                                                                                          U.S.A.
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Matches:
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Indels:
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US-08-389-564B-18/c
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Query Match:
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                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Ilm n, Marja E.
TITLE OF INVENTION: A METHOD FOR CLONING ACTIVE PROMOTERS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-AUG-15
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 19-MAR-15
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                              ADDRESSEE: Sterne, K
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REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371,2600
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 29-APR-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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PRIOR APPLICATION NUMBER: US 08/389,564
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelean ".
                                                                                          COUNTRY: U
                                                                                                                              CITY: Washington STATE: D.C.
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1100 New York Avenue,
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 Patentin Release #1.0,
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Matches:
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   Version #1.25
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RESULT 13
US-09-066-597-1/c
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
SEQUENCE 2218 base pairs
FRIGHT: 2218 base pairs
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Patent No. 6001595
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APPLICATION NUMBER: GB 86 106
FILING DATE: 30-APR-1986
ATTORNEY AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Ilm n, Marja
APPLICANT: Onnela, Maija-Leena
APPLICANT: Onnela, Maija-Leena
APPLICANT: Penttil Merja
TITLE OF INVENTION: New Promoters and Uses Thereof
TITLE OF SEOUENCES: 23
                            COMPUTER RÉADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,597
FILING DATE: Herewith
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Nw. Suite 600
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/389,564B
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STRANDEDNESS: both
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19-MAR-1990
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Matches:
Conservative:
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Query Match:
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PRIOR APPLICATION UNBER: PCT/F197/00
APPLICATION NUMBER: PCT/F197/00
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kim, Judith U.
NAME: Kim, Judith U.
1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: Of Glucose
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE:
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PRIOR APPLICATION NUMBER: US 08/980,061
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CLASSIFICATION:
                 APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                     STATE: D.C.
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5. 6011147
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                 06-JUN-1995
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13-DEC-1996
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                               US/08/466,047B
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Matches:
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Indels:
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                                                                   Version #1.25
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

US 08/389,564

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08389564B Patent No. 5989870
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Ilm n, Marja H.
APPLICANT: Penttil, Merja E.
TITLE OF INVENTION: A METHOD FOR CLONING ACTIVE PROMOTERS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 86 1060
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1716
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-260
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
No.:
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,564B
FILING DATE: 16-FEB-1995
                                                                                                                                                                      COMPUTER READABLE FORM:
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LENGTH: 2218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                      CLASSIFICATION:
                                                                                                                                                                                                            COUNTRY:
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19-MAR-1990
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Matches:
Conservative:
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RESULT 16
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Best Local Similarity:
Query Match:
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TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
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FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1716
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 19-AUG-19
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-MAR-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 29-APR-19
FILING DALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,564
APPLICATION NUMBER: 16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nakari, Tiina H.
APPLICANT: Onnela, Maija-Leena
APPLICANT: Ilm n, Marja H.
APPLICANT: Nevalainen, Kaisu Milja Helena
APPLICANT: Penttil , Merja E.
TITLE OF INVENTION: Fungal Promoters Active In
TITLE OF INVENTION: Of Glucose
NUMBER OF SEQUENCES: 34
                                                                                                    ZIP: 20005

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,047B
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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LENGTH: 2266 base pairs
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STREET: 11
                                                                                                                                                                                                                                                                                        COUNTRY:
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30-APR-1986
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19-MAR-1990
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42.00
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

19-AUG-1992

US 07/932,564

US 07/496,155

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APPLICANT: MORTYA, TATSUKI
APPLICANT: MORTYA, TATSUKI
APPLICANT: MORTYA, TATSUKI
APPLICANT: AOYAGI, KAORU

APPLICANT: SUMIDA, NAOMI

APPLICANT: MURAKAMI, TAKESHI

TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(MMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 4176
TYPE: DNA
ATTERICANT WITHTE MOREL
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09254733 Patent No. 6277596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 86 10600 FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION: NAME: REED, GRANT E. REGISTRATION NUMBER: 41,264 REFERENCE/DOCKET NUMBER: 1716.008 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: '
                                                                                                                            FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1438)..(1488)
                                                                                                                                                                                          ORGANISM: TRICHODERMA VIRIDE MC300-1
                                                              NAME/KEY: CDS
LOCATION: (1438)..(1488)
VAME/KEY: mat_peptide
LOCATION: (1489)..(3108)
                                                                                                            FEATURE
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LENGTH: 2266 base pairs
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STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/044,077 FILING DATE: 29-APR-1987
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Matches:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
                                                                                                                                                                                                                                                    ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,077C
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
                                                                                                           TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1489)..(1898)
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LOCATION: (1966)..(2662)
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LOCATION: (2725)..(3108)
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LOCATION: (1899)..(1965)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                         REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (2663) .. (2724)
                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 8075 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No : :
   MOLECULE TYPE:
                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: VA
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                     TOPOLOGY:
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                                                     nucleic acid
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                     linear
DNA (genomic)
                                single
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Matches:
Conservative:
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Indels:
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Alignment Scores:
Pred. No.:
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Best Local Similarity:
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                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0226
TELECOMMUNICATION INFORMATION:
TELEBHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6207410
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FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Ren, Dejian
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LOCATION:
                                                                                                                                                                                                                                                                                                                                               NAME: McGowan, Malcolm M. REGISTRATION NUMBER: 39,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22314-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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699 Prince Street
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157..7704
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                               Length:
Matches:
                 Conservative:
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US-10-081-935-2 (1-18) x US-09-539-879A-1 (1-8075)
                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                        Pred. No.:
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US-09-539-879A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/111,865

FILING DATE: <UNKNOWN:
APPLICATION NUMBER: US 08/374,077

FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MCGOWAN, MAICOLM M.

REGISTRATION NUMBER: 39,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 022650-264 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Zheng, Wei
Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
Calcium Channel Subunit
                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: 699 Prince Street
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FILING DATE: 31-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 157..7704
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 8075 base pairs
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Matches:
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1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18

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                                                                                    Query Match:
DB:
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APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08DA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
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                                         US-10-081-935-2 (1-18) x US-09-252-991A-9137 (1-528)
                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                      Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-9137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-9137/c
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Best Local Similarity:
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; ORGANISM: Human
US-09-058-489-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9137, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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LENGTH: 528
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                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Whitehead Institute for Biomedical Research
                                                                                                                                                                                                                                                                                          TYPE: DNA
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1 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAla 18
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44.44%
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Matches:
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Matches:
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GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15674

LENGTH: 975
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US-09-252-991A-15674
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US-09-252-991A-15702
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                                                                                                           ; NAME/KEY: unsure
; LOCATION: (571)
; OTHER INFORMATION:
US-09-252-991A-15674
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Best Local Similarity:
    Percent Similarity:
                           score:
                                             Pred. No.:
                                                                  Alignment Scores:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15702
LENGTH: 972
LENGTH: 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15702, Approximately Patent No. 6551795
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NAME/KEY: unsure
LOCATION: (669)
OTHER INFORMATION: I
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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72.22%
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50.00%
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41.00
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Length:
Matches:
Conservative:
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8728
SEQ ID NO 8728
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Query Match:
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Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                         SEQ ID NO 3
                                                                                                                                                                   TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION

FILE REFERENCE: 15966-548
CURRENT APPLICATION NUMBER: US/09/552,322
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/130,123
PRIOR FILLING DATE: 1999-04-20
PRIOR FILLING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: 60/193,203
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gould-Rothberg APPLICANT: Rastelli
                                                                                         TYPE: DNA
ORGANISM: Murinae
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                                                                                                                                    ENGTH: 1218
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RESULT 28
US-09-252-991A-15656/c
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                                                                                                                      PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15656
LENGTH: 1485
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1918
LENGTH: 1230
NAME/KEY: unsure
LOCATION: (415)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8252
                                                               FEATURE:
                                                                                  TYPE: DNA
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Acinetobacter baumannii
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  Identity of nucleotide at the above locations
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Matches:
Conservative:
Mismatches:
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  are unknown.
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; SEO ID NO 9057
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9057
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Best Local Similarity:
Query Match:
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Alignment Scores:
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                                                                                                                            GENERAL INFORMATION:
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 9057, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAKE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT ELIVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
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US-09-724-864-18
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Best Local Similarity:
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Best Local Similarity:
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SEQ ID NO 18
LENGTH: 2123
TYPE: DNA
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                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09390721
Patent No. 6197591
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                          APPLICANT: STUTZMAN-ENGWALL, KIM J.
APPLICANT: PRICE, BRENDA S.
TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED TITLE OF INVENTION: AVERMECTIN PRODUCTION
FILE REFERENCE: PC9944A
CURRENT APPLICATION NUMBER: US/09/390,721
CURRENT FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Polynucleotides, polypeptides expressed TITLE OF INVENTION: by the polynucleotides and methods for the REFERENCE: 11000,105001

CURRENT APPLICATION NUMBER: US/09/724,864

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18,
                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/100,134
EARLIER FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 6
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NAME/KEY: CDS
LOCATION: (1112)..(2317)
OTHER INFORMATION: aveR1
                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mouse
                                                                FEATURE:
                                                                              ORGANISM: Streptomyces avermitilis
                                                                                                                      ENGTH: 5045
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; NAME/KEY: CDS
; LOCATION: (2314)..(3021)
; OTHER INFORMATION: aveR2 ORF
US-09-390-721-3
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                                                                  Sequence 132, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: MACO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 5045
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: STUTZMAN-ENGWALL, KIM J.
APPLICANT: PRICE, BRENDA S.
TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED
TITLE OF INVENTION: AVERMECTIN PRODUCTION
FILE REFERENCE: PC9944A
CUURENT APPLICATION NUMBER: US/09/390,721
CURRENT APPLICATION NUMBER: US/09/390,721
CURRENT APPLICATION NUMBER: 60/100,134
EARLIER APPLICATION NUMBER: 60/100,134
EARLIER FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                        STREET: WOLF, GREENFIELD & SACKS, P.C. CITY: BOSTON
COUNTRY: USA
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Alignment Scores:
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                    Pred. No.:
                                                                     US-09-313-294A-2891
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US-09-313-294A-2891/c
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Best Local Similarity:
Query Match:
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SEQ ID NO 2891
LENGTH: 304
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                                                                                                                                                                                                                                                                          APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATT: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
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ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
                                                                                     NAME/KEY: unsure
LOCATION: 138, 178
OTHER INFORMATION:
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INFORMATION FOR SEQ ID NO: 132:
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700553448H1
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCO
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                                                                                                                                                                                                                TYPE: DNA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                ; ORGANISM: Cucumis sativus US-09-512-342-19
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                                                                                                                                            SEQ ID NO 19
LENGTH: 504
TYPE: DNA
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                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SATOH, SUSUMU
APPLICANT: MASUDA, SUSUMU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: INTERCELLULAR FLUID
FILE REFERENCE: 081356/0142
CURRENT APPLICATION NUMBER: US/09/512,342
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 38
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LENGTH: 465
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1996-02-18
PRIOR FILING DATE: 1996-07-27
NUMBER: OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08913014A
Patent NO. 6235878
GENERAL INFORMATION:
APPLICANT: Nishi, Kazunori
APPLICANT: Hikichi, Yukiko
APPLICANT: Shintani, Yasushi
TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6551795
GENERAL INFORMATION:
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SEQ ID NO 3703
LENGTH: 669
TYPE: DNA
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/913,014A
FILING DATE: 04-SEP-1997
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                         COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           STREET: 130 Wa
CITY: Boston,
STATE: MA
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David G. Conlin, ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 CTCACCCTCCAGCACCTGCTGCTGGTACTGGTCGCCGTAGGCCTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 TTCTCTTTCGGTTTTCTTTGTTGGTGAGTTTAGGCTTAGCTTCTGCG
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Sequence 9911, Application US/09252991A

Retent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

INUMBER OF SEQ ID NOS: 33142

SEQ ID NO 9911

LENGTH: 765

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
Search completed: November 13, Job time : 526 secs
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-252-991A-9931
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STRANDENESS: Doubl
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA
US-08-913-014A-7
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Pred. No.:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David G. Conlin
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/
TELECHMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 717
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Command line parameters:

-MODEL=frame+_D2n.model -DEV=xlh
-MODEL=frame+_D2n.model -DEV=xlh
-Q=/cgn2_1/USTO_50=001/US10081935/runat_04122003_134830_10487/app_query.fasta_1.391
-Q=/cgn2_1/USTO_50=001/US10081935/runat_04122003_134830_10487/app_query.fasta_1.391
-DB=EST_-OPMT=fastap_-SUFFIX=rst -MINAATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=40 -MDE=LOCAL
-OUTEMT=ptc -NOME=ext -HEAPSIZE=500 -MINLEN-0 -MAXIEN-2200000000
-USER=US10081935_@CGN_1 1_2135_@runat_04122003_134830_10487 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LOSPBLOCK=100 -LONGLOG
-DEU TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	DEFINITION	rocus	BF251103	RESULT 1
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides. 1 (bases 1 to 737)	Coccidioides immitis Coccidioides immitis	BF251103.1 GI:16931246 EST.	immitis cDNA clone CIAAC67 5' sequence, mRNA sequence. BF251103	EST418360 Coccidioides immitis spherule cDNA library Coccidioides	BF251103 737 bp mRNA linear EST 15-NOV-2001		

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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                  ProAspIleProProCysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAspGlyCys
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                                                                                                                                                                                                                                                           ThrArgLeuThrAspPheLysCysHisCysSerLysProGluLeuProGlyGlnIleThr
                                             ProThrAlaSerThrProAlaGluPheProGlyAlaGlySerAsnValArgAla-SerVa
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Location/Qualifiers
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/db_xref="taxon:5501"
/clone="CIAAC67"
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BF252723
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US-10-081-935-4 (1-194) x BF252723
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides
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Coccidioides immitis
Coccidioides immitis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
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GACCAGTGCTCCAAGGCCGGTGTCCCAATTGACATCCCACCAGTTGACACCACCGCCGCT
                                                                                 AspGlnCysSerLysAlaGlyValProIleAspIleProProValAspThrThrAlaAla
                                                                                                                            CCTTGCGTTGAGGAGGCCTGCCCCTCTCGACGCCCGTATCTCCGTCTCCAACATCGTCGTT
                                                                                                                                               ProCysValGluGluAlaCysProLeuAspAlaArgIleSerValSerAsnIleValVal
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Location/Qualifiers
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Xho1"
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 531)

Gardner, M. J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis sph
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EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: gardner@tigr.org.
Location/Qualifiers
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168 GluPheProGlyAlaGlySerAsnValArgAlaSerValGlyGlyIleAlaAlaAlaLeu
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Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides
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395 bp mRNA linear ES EST419079 Coccidioides immitis spherule cDNA library Committis cDNA clone CIAAM80 5' sequence, mRNA sequence.
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The Institute for Genomic Research
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Location/Qualifiers
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                                                                                                            GAGCCGACTCATGAGCCCACCGAGGAGCCCACTGTCGTCCCAACCGGCACTGGCGGTGGT
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 401)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Contact: Malcolm J. Gardner
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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Location/Qualifiers
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xho1"
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/mol_type="mRNA"
/db_xref="taxon:5501"
/clone="CIABB70"
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Best Local Similarity:
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 395)

Gardner, M. J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis spherule cDNA lil
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The Institute for Genomic Research
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:5501"
/clone="CIAAF11"
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/lab_host="SOLR"
/lab_host="SOLR"
/clone lib="Coccidioides immitis spherule cDNA library"
/note="Vector: pBluescript SK(-); Site_1: EcoRl; Site_2:
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Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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                                                     ProCysValGluGluAlaCysProLeuAspAlaArgIleSerValSerAsnIleValVal
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AspGlnCysSerLysAlaGlyValProIleAspIleProProValAspThrThrAlaAla 100
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/tissue_type="root"
/dev_stage="3 week"
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Dynamics/Computational Bio Scottish Crop Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                Invergowrie, Dundee, DI
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                            /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
                                                                                                                                                                                     /clone_lib="root, 3 week, 
EBro08"
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/clone="EBro08_SQ008_E05"
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                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Optic"
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Pred. No.:

1.09e-21 399.50

Length: Matches:

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Percent Similarity:
Best Local Similarity:
Query Match:
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AUTHORS
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BQ761304.1
EST.
                                                                      Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562721
Fax: 00 44 1382 562426
                                                                                                                                                                   i (bases 1 to 419)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources
                                                                                                                                                                                                                       Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooidea,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                  BQ761304
EBro06_SQ001_A05_R room
Hordeum vulgare subsp.
                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                        sequence.
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                                        est@scri.sari.ac.uk.
Location/Qualifiers
 /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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R root, 3 week,
absp. vulgare cD
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k, drought-stressed, cv Optic
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cv Optic, EBro06
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BQ499065 1 GI:2-
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Paracoccidioides brasiliensis
Paracoccidioides brasiliensis
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (Dases 1 to 311)
Goldman, G.H., Marques, E.R., Ribeiro, D.C.D., Bernardes, L.A., Puccia, R., Travassos, L.R., Nobrega, F.G., Nobrega, M.P., Savoldi-Barbosa, M., Semighini, C.P. and Goldman, M.H.
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US-10-081-935-4 (1-194) x BQ761304
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| ATGAAGTTCTCCACCACTCTGATTGCCTTCGTTGCCGCCGGCCTCGCCAGCGCCCAGCCTG
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/db xref="taxon:112509"
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/dev_stage="3 week"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. After two weeks in control conditions the seedlings were raised above the hydroponic solution for 3 hours daily. N.B. This library has been superseded by EBro08. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
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56.15%
37.34%
GI:24452039
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Paracoccidioides brasiliensis
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                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 667)

1 (chambergo, F. S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P., Elucidation of the metabolic fate of glucose in the filamentous fungus Trichoderma resesi using expressed sequence tag (EST) analysis and cDNA microarrays

3. Biol. Chem. 277 (16), 13983-13988 (2002)
                                                                                                           Contact: El-Dorry, Hamza
Department of Biochemistry
Institute of Chemistry. Un:
                           Email: dorry@iq.usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotic Cell, (2002) In press Contact: Gustavo Henrique Goldman Laboratory of Molecular Biology Universidade de Sao Paulo - USP - FCFRP Av do Cafe S/N, CEP: 14040-903, Ribeirao
                                                                                             Avenida Professor Lineu
                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
BM077163
 FORWARD: Universal M13
                  PCR PRimers
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                                              (55) 11-38183848
(55) 11-38183848
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/mol type="mRNA"
/db_xref="taxon:121759"
/clone lib="pb0001"
88 c 59 g 91 t
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Prestes, 748, Sao
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                                                                                                    -------GluGluProThrAla------ValProThrGlyThrGlyGly
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/dev_stage="18 hr Glycerol-grown culture"
/lab_host="E.coli SOLR cells (kanamycin resistant)"
/clone_lib="TrEST-A"
/clone_lib="TrEST-A"
/note="Vector: pBluescript_SK(+); Site_1: EcoRI; Site_2:
XhoI; anamorph=Trichoderma reesei; Cloned unidirectionally
Site_1 coloned into EcoRI site of
pBluescript. Primer: Oligo (dT). Average insert size: 1,2
kb; Uni-ZAP XR Vector system -5' adaptor sequence:
S'GAATTCGGCACGAG3' -3' adaptor sequence:
5'CTCAAGTTTTTTTTTTTTTTTTTT3'"
98 a 266 c 188 g 115 t
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/db_xref="taxon:51453"
/clone="Tr-A0723"
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grisea cDNA clone mgcs006xB09 5',
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BM866652.1 GI:19234334
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Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7
Tel: 979 845 483
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 564)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromatogram file of this sequence is available, see contact person Best nr hit (April. 22, 2003) gb|EAA29323.1| predicted protein [Neurospora crassa] 55 6e-07 PCR PRimers
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BACKWARD: T7 primes
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                                                                                                                                               100
                                                                                                                                          /clone_lib="Magnaporthe grisea CS Uni-Zap XR Library"
/clone="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI
; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Conidial library. Point inoculation of Guyll at center of
oatmeal agar plate. Conidia were harvested after two weeks
of growth. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."

242 c 128 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d-ebbole@tamu.edu
                                                                                                                                                                                                                                                                                                                                            /sex="Mat1-2 hermaphrodite"
/cell_type="conidia"
/clone_lib="Magnaporthe ori
                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:148305"
/clone="mgcs006x809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            strain="Guy11"
 1.98e-06
202.50
47.42%
32.99%
19.79%
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REFERENCE
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VERSION
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BACKWARD: T7 primer
                                                                                          Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) gb|EAA29323.1| predicted protein
                                                                                                                                                   Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
                                                       (Neurospora crassa) 51 8e-06 PCR PRimers
                                                                                                                                                                                                             Department of Plant Pathology & Microbiology
Texas A&M University
                                                                                                                                                                                                                                                      Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                  Ebbole,D.J., Yuan,J., Thomas,T.L., ,K. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnaporthe
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                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                             Expressed
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Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnaporthe grisea (anamorph: Pyricularia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACGGCGAGGCCCTGTGCAAGAACGTCCCCACCGCTGTTCCTACCTCCT------CC
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Percent Similarity:
Best Local Similarity:
Query Match:
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Seq primer: T3
                                                                                                                                                                                                          - ACCTCTGCTGCCTCTCCCACCGCTTCCCCCACCAGCACCAGCGGCGGCGGCAGCAGGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                               GACCTCTCCAAGGCTGCCACCAACGGCGAGGCCCTGTGCAAGAACGTCCCCACCGCTGTT 242
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                                                                            eProGlyAlaGlySerAsnValArgAlaSerValGlyGlyIleAlaAlaAlaLeuLeuGl 189
                                                                                                                                  CAGCGGCACCAGCGGC-
                                                                                                                                                          oThrGlyThrGlySerPheThrValThrGlyArgProThrAlaSerThrProAlaGluPh
                                                                                                                                                                                                                                           sGluProThrGluGluProThrAlaValProThrGlyThrGlyGlyVal-----Pr 149
                                                                                                                                                                                                                                                                                      TCGGCCTCGGCCAGCACCATGCCCTCCATGTCGACTGGCGTCCCCAAGACCAACGGC
                                                                                                                                                                                                                                                                                                                           aGluProThrGluGluProThrAlaGluProThrAlaGluProThrAlaGluProThrHi 131
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/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI
; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Conidial library. Point inoculation of Guyll at center of
oatmeal agar plate. Conidia were harvested after two weeks
of growth. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredphrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."

83 a 233 c 132 g 105 t
                                                 GGCTCTGGCGCCTCCGCC---GCCACTATCGGC-----GCTGCTGCTCTTCTTGG
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/sex="Mat1-2 hermaphrodite"
/cell_type="conidia"
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/mol_type="mRNA"
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46.70%
33.52%
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomy.
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 952)
Chanados T Couroux.P., Harris,L.
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Agriculture and Agri-food Canada
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A cDNA library prepared from
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J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A., Sprot
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(613) 759-1701
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211 c 288 g 226 t 5 others
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/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFC_ECORC_Fusarium_graminearum_complex_substrate"
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sequence.
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Fungal Genet. Biol. 38 (2), 187-197 (2003)
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                     688 bp mRNA linear EST 06-MAY-2003 mgmy002xP06f.b Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe grisea cDNA clone mgmy002xP06 5', mRNA sequence.
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On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ
Department Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7
Tel: 979 845 4831
                                                                                                                                                           Ebbole, D.J., Yuan, J., Thomas, T.L., K. and Dean, R.A.
                                                                                                                                                                                                                                                  Magnaporthe grisea
                                                                                                         Unpublished
                                                                                                                                         Expressed sequence tags from the
                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; So
Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                 Magnaporthe grisea (anamorph:
                                                                                                                                                                                                                                                                                                      BM872390.2 GI:30406827
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|||...: |||||||| ...||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTTGACCGAAGCTTGCCAGGTTGATGACCTACTCAAGGCCCAGAAGGCTGCCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspPheLysCysHisCysSer------LysProGluLeuProGlyGlnIleThrPro
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Gaps:
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                                                                                                                                         rice blast fungus, Magnaporthe
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                                                                                                                                                                              Bobrowicz, P.,
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                                                                                       gi:19240072
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ORIGIN
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О
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138 ThrAlaValProThr------GlyThrGlyGlyGlyValProThrGlyThrGlySer
                                                                                                                                                                                                        103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 979 845 6483
Email: d-ebbble@tamu.edu
Chromatogram file of this sequence is available, see contact person
;Best nr hit (April. 22, 2003) gb|EAA30838.1| predicted protein
[Neurospora crassa] 49 7e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR PRimers
FORWARD: T3 primer
                                                                                                                                                                                                                                                                                          CysSerLysAlaGlyValProlleAspIleProProValAspThrThrAlaAlaProGlu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheLysCysHisCysSerLysProGluLeuProGlyGlnIleThrProCysValGluGlu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAspGlyCysThrArgLeuThrAsp 45
                                                                                                                                                                                                                                                                                                                                                                                     AlaCysProLeuAspAlaArgIle-----SerValSerAspIleValValAspGln---
                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGTGCCTGTGCGACAAACCCGACTATCGCAACGGTCTGAAAGACTGTGTGACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeulleAlaLeuValAlaAlaGlyLeuAlaSerAlaGln---LeuProAspIleProPro 25
                                                                 TCAGCTCCTGCATCTACCTCCTGCTGCTTCGACAACACCTAGCTCAACGTCAGCGTCG
                                                                                                                                                                                                   ProSerGluThrAlaGluProThrAlaGluProThrGluGluProThrAlaGluProThr 122
                                                                                                                                                                                                                                                                                                                                          AGCTGTGGCGCTGATGCAACAGCAGTCCACGCTGCATTGAACACATACGTCGATGCTGTC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCGGGCAAGGTTGCTTCAACAGCATGAAGGGCACATTGGGTTGTGCTCCT---GCCGAC 121
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/sex="Wat1-2 hermaphrodite"
/sex="Wat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe_grisea_MY_Uni-Zap_XR_Library"
/clone_lib="Magnaporthe_grisea_MY_Uni-Zap_XR_Library"
/clone_lib="Magnaporthe_grisea_MY_Uni-Zap_XR_Library"
/clone_lib="mycelium"
/clone_lib="mycelium"
/clone_lib="mycelium library. Scont side has T3 primer and
predominantly_5' reads. T7 primer on XhoI side of insert.
Minimal medium mycelium library. Sequences were processed
by one of two methods. Where a full-length alignment to
the M. grisea genome_sequence_was_available_the_EST_
has a primer a full-length alignment to
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224 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Magnaporthe/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                          GluProThrAlaGluProThrHisGluProThrGluGluPro 137
                                                                                                                                                          - CCAGCATCGACTCCGCCTCATTCTACCTCGGCGCCACCAACC
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BM872513
Alignment Scores:
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On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7
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Seg primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: d-ebbole@tamu.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebbole, D.J., Yuan, J., Thomas, T.L.,
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979 845 6483
                                                                                        /clone="mgmy003xM10"
/sex="Mgmt1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
/clone_lib="Magnaporthe grisea To primer on Xhol side of insert
/clone_lib="Magnaporthe grisea"
/clone_lib="Magnaporthe grisea To xhol side of insert
/clone="Minimal Red of the grisea My Colored Will-length alignment to
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                                                                                                                    Magnaporthe grisea
Eukaryota; Fungi; /
Contact: Ebbole DJ
Department of Plant Pathology
Texas A&M University
                                                                                                                                                       CD035585.1
EST.
                                  Unpublished
                                                                                                        Sordariomycetes incertae
                                                                                                                                          Magnaporthe grisea (anamorph: Pyricularia
                                                           Expressed sequence tags
                                                                        bbole,D.J., Yuan,J.,
K. and Dean,R.A.
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            & Microbiology
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                                                                                 Lu,G., Bhatterai
                                                                                                       Magnaporthe.
                                                           Magnaporthe
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FORWARD: T3 primer
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Tel: 979 845 4831
Fax: 979 845 6483
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 ProGluProSerGluThrAlaGluProThr-----
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US-10-081-935-4 (1-194) x CD035585
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Seg primer: T3.
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Chromatogram file of this sequence is available, see contact polynomatogram file (2, 2003) gb|AAN64312.1| MAC1 interacting protein 1; AC11 [Magnaporthe gri. . . 208 6e-53]
                                                                                                                                                                                                                                                                                                          CAGCAGGCCAAGATGTTTGCCGCCGTCGAGAGCTGCGTGCAAAAGAGCTGCCCAGAGTCT
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                                                                                                                                                     GAGTTCCAAAAGACCÁTTGACGGATCTGACAAGGTCTGC---ACGTGCGCTTCTGGAGGT
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/dev_stage="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/clone_lib="
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/sex="Mat1-2 and Matl-1 mixted culture"
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/db_xref="taxon:148305"
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Center For Genetic Resource Ini
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-APR-2000) Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope
- Web : www.genoscope.cns.fr)
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Genome Res. 10 (7), 939-949 (2000)
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Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)
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Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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GSS; genome survey sequence.
Tetraodon nigroviridis
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                                                                                                                                                                                            /clone_lib="C"
/note="Genoscope
253 c 248
                                                                                                                                                                                                                                                               organism="Tetraodon nigroviridis"
|mol_type="genomic DNA"
|db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                  clone="014N06"
                                   0.00181
168.00
51.16%
37.21%
16.42%
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Conservative:
Mismatches:
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survey sequence T7 end of clone
aodon nigroviridis, genomic survey
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42
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86

AlaGlyValProIleAspIleProProValAspThrThrAlaAlaProGluProSerGlu

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ω
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
On Mar 7, 2002 this sequence version replaced gi:19233888.
Contact: Ebbole DJ
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 4833
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person ;Best nr hit (April. 22, 2003) gb[AAN64312.1] MAC1 interacting protein 1; AC11 [Magnaporthe gri. . . 192 3e-48
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mgcs005xCl3f.b Magnaporthe grisea CS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcs005xCl3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 567)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P.,
,K. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM866206.2 GI:30394891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magnaporthe grisea (anamorph: Pyricularia
                                                                                                                                                                                                                                                                                                                                                                         Plate: mgcs005
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGGTGAACCAACGGGT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyValProThrGlyThrGlySerPheThrValThrGlyArgProThrAlaSerThr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGGTCAACCAACGATCAACCAACGATCAACCAACGGGTCAACCGGCAGGTCAGCCA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrAlaGluProThrHisGluProThrGluGluProThrAlaValProThrGlyThrGly 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrAlaGluProThrAlaGluProThrGluGluProThrAlaGluProThrAlaGluPro 125
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/clone_libe="Magnaporthe grisea CS Uni-Zap XR Library"
/clone_libe="Magnaporthe grisea CS Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI
; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Conidial library. Point inoculation of Guy11 at center of
oatmeal agar plate. Conidia were harvested after two weeks
of growth. Sequences were processed by one of two methods.
where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                         /sex="Mat1-2 hermaphrodite"
/cell_type="conidia"
                                                                                                                                                                                                                                             /db_xref="taxon:148305"
/clone="mgcs005xC13"
                                                                                                                                                                                                                                                                                  /strain="Guyll"
                                                                                                                                                                                                                                                                                                                     organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                  primer
                                                                                                                                                                                                                                                                                                  type="mRNA
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Percent Similarity:
Best Local Similarity:
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                             Contact: Frances Trail
Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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                                                                                                                                                                                                                                                                                                                                                      BU064230
Fgr_4_F04_T3 |
sequence.
BU064230
                                                                                                                                                                                                                                              Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                1 (bases 1 to 607)
Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamor
                                                                                                                                                                                                                                                                                                      Gibberella zeae
                                                                                                                                                                Fungal Genet. Biol.
                                                                                                                                                                                   Fusarium graminearum)
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4 row:
               trail@msu.edu
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Hypocreales; Nectriaceae; Gibberella.
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/mol type="mRNA"
/strain="NRRL 31084"
/db xref="taxon:5518"
/clone_lib="Nitrogen-st
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Trail, F., Xu,J.-R., San Miguel, P., Halgren, R.G. and Kistler, H. Analysis of expressed sequence tags from Gibberella zeae (anan Fusarium graminearum)
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Department of Plant Biology
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                        ValArgAlaSerValGlyGlyIleAlaAlaAlaLeuLeuGlyLeuAlaAlaTyr 193
                                                                                                                                              GluProThrAlaValProThrGlyThrGlyGlyGlyValProThrGlyThrGlySerPhe
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/clone_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"
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/mol_type="mRNA"
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sequence.
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East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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Department of Plant Biology
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/mol_type="mRNA"
/strāin="NRRL 31084"
/db_xref="taxon:5518"
/clome_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI;
/note="Vector: Uni-ZapII; Site_1: EcoRI;
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Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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sequence.
BU064409
                       21 ProAspIleProProCysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAspGlyCys 40
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Analysis of expressed sequence tags
Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197
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GCCGACGTCCCCAAGTGCGCCATTCCTTGCCTCGACAAGGCCATCGCCAGCGAGACCAGC
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4 row: M column: 16
Location/Qualifiers
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/note="Vector: Uni-ZapII; Site_1: EcoRI;
239 c 155 g 126 t
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/strain="NRRL 31084"
/db_xref="taxon:5518"
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                                                                                                                                                                                            Department of Plant Biolog
Michigan State University
East Lansing, MI 48824, US
Tel: 517 432 2939
Fax: 517 353 1926
                                                                                                                                                                                                                                              Contact: Frances Trail
Department of Plant Biology
                                                                                                                                                                   Email: trail@msu.edu
Plate: 1 row: E co
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Analysis of expressed sequence tags
Fusarium graminearum)
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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241 c 155 g 129 t
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Contact: Frances Trail
Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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(bases 1 to 696)

Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistler, H. Analysis of expressed sequence tags from Gibberella zeae (anamy Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
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/mol type="mRNA"
/strain="NRRL 31084"
/db_xref="taxon:5518"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

(bases 1 to 699)

Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistl Analysis of expressed sequence tags from Gibberella zeae Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
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Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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/mol_type="mRNA"
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/db_xref="taxon:5518"
/clone_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI;
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Trail F. Xu.J.-R., San Miguel, P., Halgren, R.G. and Analysis of expressed sequence tags from Gibberella Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Plant Biology Michigan State University
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Plate: 5 row: K column: 14.
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 'bases 1 to 718'
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                                                                                                                      TGTGACAAGACCGACCTCGCCTGTGTCTGCAAGGGCTTCAGCGCTGTCCGATCCAAGGCT 259
                                                                                                                                                                                  GCGACGTCCCCAAGTGCGCCATTCCTTGCCTCGACAAGGCCATCGCCAGCGAGACCAGC
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                             ValAspGlnCysSerLysAlaGlyValProIleAspIleProProValAspThrThrAla
                                                                                                                                                     ThrargLeuThraspPheLysCysHisCysSerLys---ProGluLeuProGlyGlnIle 59
                                                                                                                                                                                                                                               ATGAAGTACTCCGTCGCTTTCGTTGCTCTCGCCGCTGTTGCCGCTCAGGCTCAGTCTCTT 139
                                                            ACCTCTTGTGTCATTGACGAGTGTGGTACCGAC-----GTTGCCATCAACGAGGTC---
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/clone_lib="Nitrogen:starved mycelia"
/note="Vector: Uni-ZapII; Site_1: Ecof
/note="Vector: 168 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gibberella
/mol_type="mRNA"
/strain="NRRL 31084"
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Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
Tel: 517 432 2939
Fax: 517 353 1926
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Gibberella zeae
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Plate: 6 row: C column: 13
Location/Qualifiers
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Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamorph
Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
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ProAspIleProProCysAlaLeuAsnCysPheValGluAlaLeuGlyAsnAspGlyCys 40
                                                 MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAlaGlnLeu 20
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                                                                                                                                                                                                                                                                  /db_xref="taxon:5518"
/clone_lib="Nitrogen-starved mycelia"
/clone_lvector: Uni-ZapII; Site_1: EcoRI;
/note="vector: Uni-ZapII; Site_1: EcoRI;
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/mol_type="mRNA"
/strain="NRRL 31084"
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                                                                                                                                                                                                          Eastern Cereal and Oilseed Research Agriculture and Agri-food Canada Bldg. 20, Central Experimental Farm,
                                                                                                                                                                                                                                                                                                                                                                                        Gibberella
Gibberella
                                                                                                                                                                                                                                                   Unpublished
Contact: Watson, Robert.J.
                                                                                                                                                                                                                                                                            A cDNA library prepared complex plant substrate
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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                                                                                                                                                                    (613) 759-1701
                                                                                                                                                                                 (613)
                                                                                                                                         watsonrj@agr.gc.ca.
Location/Qualifiers
/db_xref="taxon:5518"
/clone="Fg08 01h09"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFC_ECORC_F
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                                                                                   /mol_type="mRNA"
/strain="DAOM 180378"
                                                                                                               'organism="Gibberella
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                                                                                                                                                                     Fg08_01h09_R Fg08_AAFC_ECORC_FUBARTIUM_graminearum_complex_substrate Gibberella zeae cDNA clone Fg08_01h09, mRNA sequence. CD458020 CD458020 CD458020.1 GI:31372760
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycet Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. 1 (bases 1 to 867). Watson,R.J., Heys,R., Chapados,J., Couroux,P., Harris,L.J., J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A., Sprot
                                                                                                                       Gibberella
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
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/clone="F908_01h09"
/tissue_type="Mycelium"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli_DH10B"
/clone_lib="F908_AAFC_ECORC_Fusarium_graminearum_complex_s
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/mol_type="mRNA"
/strain="DAOM 180378"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromatogram file of this sequence is available, see contact p; Best nr hit (April. 22, 2003) gb[AAN64312.1] MAC1 interacting protein 1; ACI1 [Magnaporthe gri. . . 179 3e-44
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Contact: Ebbole DJ
Department of Plant Pathology
Texas A&M University
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BACKWARD: T7 prime:
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PCR PRimers
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Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
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Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: T3.
                                                                                                                                                                                      /sex="Max1-2 hermaphrodite"
/sex="Max1-2 hermaphrodite"
/cell type="conidia"
/clone lib="Magnaporthe grisea CS Uni-Zap XR Library"
/clone wester yellowseriptsK: Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Conidial library. Point inoculation of Guyll at center of oatmeal agar plate. Conidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredbrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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clone="mgcs013xP19"
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                                                                                                                              Department of Plant Biology
Michigan State University
East Lansing, MI 48824, USA
                                                                                                                                                                                                Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminearum)
Fungal Genet. Biol. 38 (2), 187-197 (2003)
                                                                                                                                                                                                                                    1 (bases 1 to 696)
Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistler, H.C
                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes, Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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Gibberella
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                                                                                                       t Lansing, MI 4
: 517 432 2939
: 517 353 1926
                                                                    trail@msu.edu
5 row: D column: 02
Location/Qualifiers
/strain="NRRL 31084"
/db_xref="taxon:5518"
/clone_lib="Nitrogen-starved
                                               organism="Gibberella
                                    mol_type="mRNA"
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Percent Similarity:
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RYA linear EST 03-JUN-2003

F909_03i13_A F909_AAFC_ECORC_FUSArium_graminearum_simple_substrate
Gibberella zeae cDNA clone F909_03i13, mRNA sequence.
                                    1 (bases 1 to 822)
Watson,R.J., Heys,R., Couroux,P., De Moors,A., Harris,L.J., Hattori,J., Lacroix,C., Masotti,M., Ouellet,T., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
                                                                                                                                                             Gibberella
Gibberella
                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
substrate
                   A cDNA library prepared from Fusarium
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottaw:
nValArgAlaSerValGlyGlyIleAlaAlaAlaLeuLeuGlyLeuAlaAlaTyr 193
                           GCCCGCCACCAGCACCCCCGCCGCCACCCCTACCAAGGGTCCC---GAGCAGGCCAA
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                                                       eThrValThrGlyArgProThrAlaSerThrProAlaGluPheProGlyAlaGlySerAs
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(613) 759-1701
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Location/Qualifiers
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267 c 195 g 172 t 4 others
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/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/lone_"lb="F909_AAFC_ECORC_Fusarium_graminearum_simple_su
/clone_"lb="F909_AAFC_BCORC_Fusarium_graminearum_simple_su
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/mol_type="mRNA"
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/clone="Fg09_03i13"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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East Lansing, MI 48824, US
Tel: 517 432 2939
Fax: 517 353 1926
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Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamorph
Fusarium graminearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Frances Trail
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/db_xref="taxon:5518"
/clone_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI;
/note="Vector: 143 g 111 t
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/mol_type="mRNA"
/strain="NRRL 31084"
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arved mycelia Gibberella zeae cDNA, mRNA
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Department of Plant Biology
Michigan State University
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AU284313 Dictyostelium discoideum FC (H.Urushihara) Dictyostelium discoideum FC (H.Urushihara) Dictyostelium discoideum cDNA clone FC-AK17 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-298-53-4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Tsukuba
1-1-1 Tennoudai, Tsuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Muramoto, T., Suzuki
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/clone_lib="Dictyostelium
164 c 62 g 157
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/mol_type="mRNA"
/strain="KAX3"
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clone="FC-AK17"
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1 (bases 1 to 643)

Trail, F., Xu, J.-R., San Miguel, P., Halgren, R.G. and Kistler, H.C. Analysis of expressed sequence tags from Gibberella zeae (anamor Fusarium graminearum)
                                                                                                                                                                                                                                                                     Department of Plant Biology Michigan State University
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                                                                                                                                                                                                                                 Lansing, MI 48824,
517 432 2939
517 353 1926
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                                                                                                                                                                                                                         trail@msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D22_T3 Nitrogen-starved
                                                                                                           a
                                                                                                      /organism="Gibberella zeae"
/mol type="mRNA"
/strāin="NRRL 31084"
/db_xref="taxon:5518"
/db_xref="taxon:5518"
/clone_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"
240 c 147 g 125 t
                                                                                                                                                                                               row: D column: 22.
Location/Qualifiers
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42.42%
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Matches:
Conservative:
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AUTHORS
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                                                                                                                           Unpublished
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/organism="Gibberella
             . 874
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Tinker, N.A.
A cDNA library prepared from
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CD459301
                                                                                                                                             Contact: Watson, Robert.J.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada
                                                                                                                                                                                                                                                                                                                      Watson, R.J., Heys, R., Chapados, J., Courous, J., Lacroix, C., Ouellet, T., Robert, L.S.,
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                    complex plant substrate
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                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 874)
                  (613) 759-1655
(613) 759-1701
l: watsonrj@agr.gc.
                                                                                                                        20, Central Experimental
Location/Qualifiers
                                                                                                                                                                                                                                                                            Fusarium
                                                                                                                      Farm, Ottawa,
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t,L.S., Singh,J.A., Sprott,
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Best Local Similarity:
Query Match:
DB:
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ORIGIN
Search completed: December Job time: 1943 secs
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                                                                                                                                                                                  gProThrAlaSerThrProAlaGluPheProGlyAlaGlySerAsnValArgAlaSerVa 180
                                                                                                                                                                                                                        ACCCACGGGAACCTCTGGCGGCGC-----GGCGGCGGCAGCGGCACCACTGGCGGTGC
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                                                                          GTGHCCCCTCGCCATTATTGCTGCKGCTATCGCT
                                                                                                            lGlyGlyIleAlaAlaAlaLeuLeuGlyLeuAla 191
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/strain="DAOM 180378"
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/tissue_type="Mycelium"
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/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFC_ECORC_Fusarium_graminearum_complex_s
ubstrate"
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196 c 275 g 197 t 15 others
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
I (bases 1 to 395)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis sph
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395 bp mRNA linear EST 15-NOV-2001
EST418539 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAFI1 5' sequence, mRNA sequence.
                                                            Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                             Tel: 301 838 3519 Fax: 301 838 0208
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Gardner, M.J. and Kirkland, T.
                                                                                                                                                                                                                 Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 3519
Fax: 301 838 0208
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The Institute for Genomic Research
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Malcolm J. Gardner
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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Generation of ESTs from Coccidioides immitis spherule cDNA li
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Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                            99
Paracoccidioides brasiliensis
Paracoccidioides brasiliensis
Bakaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (bases 1 to 311)
Goldman,G.H., Marques,E.R., Ribeiro,D.C.D., Bernardes,L.A., Puccia,R., Travassos,L.R., Nobrega,F.G., Nobrega,M.P., Savoldi-Barbosa,M.
Semighini,C.P. and Goldman,M.H.
The Paracoccidioides brasiliensis EST genome project
                                                                                                                                        BQ499065 311 bp mRNA lir
EST08290 pb0001 Paracoccidioides brasiliensis
BQ499065
BQ499065.1 GI:24452039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 301 838 3519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Euonygenales; mitosporic Onygenales; Coccidioides. 1 (Dases 1 to 737)
Gardner, M.J. and Kirkland, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Malcolm J. Gardner
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301 838 0208
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Location/Qualifiers
1. .737
                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="spherule"
/lab_host="$OLR"
/clone_lib="Coccidioides immitis apherule cDNA library"
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2
Xho1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Coccidioides
/mol_type="mRNA"
/db_xref="taxon:5501"
/clone="CIAAC67"
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f ESTs from Coccidioides
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100.0%; Pred. No. 1.6e-05;
tive 0; Mismatches 0;
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Pred. No. 1.6e-05;
Mismatches 0;
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sis cDNA,
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                                                                                                                                                                             mRNA sequence.
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Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.scri.k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F. M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Contact: Gustavo Henrique Goldman
Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil
Email: ggoldman@usp.br.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
BQ761304
BQ761304.1 GI:21969776
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Waugh R, Marshall DF
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            71
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/note="Vector: pSPORT1; Site 1: Sal 1; Site 2: Not 1; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. After two weeks in control conditions the seedlings were raised above the hydroponic solution for 3 hours daily. N.B. This library has been superseded by EBroOB. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
                                                                                                                                                                                                                                          /db_xref="taxon:112509"
/clone="EBroO6_SQ001_A05"
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, drought-stressed, cv
_EBroO6"
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/mol_type="mRNA"
/db_xref="taxon:121759"
/clone_lib="Pb0001"
88 c 59 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Optic"
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Pred. No. 0.07
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RESULT 9
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Best Local Similarity
Matches 40; Conserv
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    sequence.
BQ767421
                              BQ767421
EBro08_SQ008_I22_R root,
Hordeum vulgare subsp. vu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Invergowrie, Dundee, DD2 5DA,
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
Location/Qualifiers
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
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Genome Dynamics/Computational Biology
Scottish Crop Research Institute
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a 217 c 119 g 111 t
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                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Optic"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="EBro08_SQ008_E05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Hordeum vulgare
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ot, 3 week,
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                               vulgare cDNA clone
                              602 bp mRNA linear EST 26-JUL-2002
3 week, drought-stressed, cv Optic, EBro08
ulgare cDNA clone EBro08_SQ008_I22 5', mRNA
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c, drought-stressed, cv Optic, EBro08
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Yarrowia lipolytica
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.

1 (bases 1 to 994)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Belotin-Fukuhara, M., Bon, E., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuweglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Malpertuy, M., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 602)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished
                    Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1.
Yeast species for molecular evolution studies
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                     AL411113.1 GI:12180209
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Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotlan
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                 Yarrowia lipolytica,
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                                                                                                                                                                                                                                                                                                                                                                                                    of clone AWOAA009A12 of library AWOAA from la lipolytica, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          est@scri.sari.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:112509"
/clone="EBro08 SQ008 I22"
/tissue_type="Toot"
/dev_stage="3 week"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="root, 3 week, drought-stressed,
EBro08"
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/cultivar="Optic"
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                                                                                                                                                       559 bp DNA linear GSS 12-OCT-2002
CH230-477F24.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
BZ235140
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Zhao, S., Shattyn, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
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                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4952"
/clone==AAWAAA009A12"
/clone==AAWAAAAA"
/clone=Tib="AAWAAA"
/notes==end : T3"
<653. .>969
/notes=sinilar to Saccharomyces cerevisiae ORF YPL123c [
similarity to ribonuclesses ]
putative frameshift(s)"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
             Casaregola, S., Neuveglise, C., Lepingle, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CLIB 89"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                      FEBS Lett. 487 (1), 95-100 (2000)
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Rattus norvegicus
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76.6%;
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Genoscope.
 (bases 1 to 994)
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9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: schao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 477 row: F column: 24
Class: BAC ends.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
: eurosids II; Brassicales; Brassicaceae; Brassica.
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BNAF0225E Mustard flower buds Brassica rapa cDNA clone F0225, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell type="Brain"
/clone_lib="CHORL-230 Segment 2"
/note="Vector: pTARBACL.3; Site_1: Mbo1; Site_2: Mbo1;
CHOR1-230 Rat (BN/SSNHed/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H.,
Hwang,I. and Cho,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lim,C.O., Kim,M.G., Hwang,I. and Cho,M.J.
Plant Molecular Biology and Biotechnology Research Center
Email: pmbbrc@nongae.gsnu.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27.4; DB 29; Length 559;
Pred. No. 2.3e+02;
0; Mismatches 11; Indels 0.
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/clone="F0225"
/clone lib="Mustard flower buds"
/note="Devel stage = flower bud "
110 c 67 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                1. .559
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10116"
/clone="CH230-477F24"
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/strain="pekinensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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1 Similarity 75.6%;
34; Conservative (
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L38010.1 GI:887186
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CA766669.2
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                                        ORGANISM
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AF53-Rpf 12 F09 T7 035.abl IRRI Drought Stress Panicle Library Oryza sativa (indica cultivar-group) cDNA clone C0004353 5' similar CA766669
                                                                                                                                                BI519263 1615 bp mRNA linear EST 29-AUG-2001 603062017R1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211149 3',
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                              ö
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1615)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                      Email: cgapber-general inflago.
Tissue Procurement: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 06
High quality sequence stop: 76.
Location/Qualifiers
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                              Gaps
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  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                    7 GTTCTCTCTCTATCTTCTTCTCGACGATGCCGGCTTC 46
 Score 27.2; DB 14;
Pred. No. 2.4e+02;
0; Mismatches 8;
                                                      6 GTTCTCTCACGCTCTCATCGCTCTCGTCGCCGGCCTC
                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                           BIS19263
BIS19263.1 GI:15344055
52.3%;
                                                                                                                                                                                                                                 Homo sapiens (human)
                            32; Conservative
                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                  Homo sapiens
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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AUTHORS
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CA766669
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehratcoideae; Oryzeae; Oryza, Liliopsida; Poales; Poaceae;
Ehratcoideae; Oryzeae; Oryza, Lafitte, R., Wen, J., Rudd, S. and
Bruskiewich, R.M.
IRI Drought Stress Panicle cDNA Library
IN Dupublished
On Dec 2, 2002 this sequence version replaced gi:25995924.
Contact: Richard Bruskiewich
Blometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS;
http://www.iris.irri.org): DD204352
Assignment of putative function to the sequence by S. Rudd of the
Munich Information Center for Protein Sequences (http://mips.gsf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Panicles"
/dev_stage="Flowering"
/dev_stage="Flowering"
/clone lib="IRRI Drought Stress Panicle Library"
/clone lib="IRRI Drought Stress Panicle Library"
/note="Vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (wall watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."
Is 153 c 139 g 139 t 1 others
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Spencer, D. H., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 559 / Organism="Noryza sativa (indica cultivar-group)" / Mol_type="mRNA" / Cultivar="IR64" / Cultivar="IR64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%; Score 26.6; DB 14; 71.4%; Pred. No. 3.9e+02;
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/clone="C0004353"
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Location/Qualifiers
GI:27548712
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Best Local Similarity 71.4
Matches 35; Conservative
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Gaps

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/db_xref="GAB1:44280"
/db_xref="GAB1:44280"
/db_xref="Taxon:112509"
/clone="HS01B12"
/tissue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="xL10-Gold"
/lab_host="xL10-Gold"
/clone_lib="HS"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukartyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
    /clone_lib="RPCI-11 Human Male BAC Library" hote="Vector: pBACE3.6; Site 1: ECOR1; Site 2: ECOR1; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoR1 and ECOR1 Methylase. Size selected DNA was cloned into the ECOR1 Methylase. Size selected DNA was cloned into the Labeled of vector and ECOR1 sites" 30 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA linear EST 15-JUL-2002 vulgare cDNA clone HS01B22
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                                                                                                                                                                                                                                                                                                                         Contact: Stein Nils
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 447 Std Error: 0.00
Plate: 1 row: B column: 22
                                                                                                                                                                                                          Length 1044;
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    .447
    /organism="Hordeum vulgare"

                                                                                                                                                                                                                                                      16; Indels
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                                                                                                                                                                                                       50.8%; Score 26.4; DB 28;
69.2%; Pred. No. 4.9e+02;
ive 0; Mismatches 16;
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Pred. No. 4.9e+02;
0; Mismatches 13;
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BQ662215
BQ662215.1 GI:21803348
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/cultivar="barke"
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                                                                                                                                                                                                                                                    36; Conservative
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Best Local Similarity 72.3
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T7.
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                           295
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                                                                                                                                                                                                          Query Match
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BQ662215/c
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availablity, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web_Server:
Plate: 963 row: J column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 16-JUL-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1044)
Mahahiras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ743420

1044 bp DNA linear GSS 16-JUL-HS_5387_B1_E08_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=963 Col=15 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                          /db xref="taxon:287"
/clone="pacs2-164_492"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CAGTICICICACGCTCTCATCGCTCTCGTCGCTGCCGCCTCGCCAGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                              'organism="Pseudomonas aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26.6; DB 29
Pred. No. 4.1e+02;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
|mol_trype="genomic DNA"
|/mol_trype="genomic DNA"
|/dD_xref="taxon:9606"
|/clone="Plate=963 Col=15 Row=J"
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Email: craymond@u.washington.edu
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                            163 t
                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="2-164"
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Location/Qualifiers
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AQ743420.1 GI:5520942
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Best Local Similarity 71.4%;
Matches 35; Conservative (
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                                                                                                                                                                                                                                                                                                                                                            299 C
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AQ743420/c
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Gaps

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EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
; Triticeae; Hordeum.
; Triticeae; Lo 627).
                                          Ostariophysi; Cypriniformes
                                                                        1 (bases 1:0 522)
Lee, S., Ruan, H., Ma, W., Xu, M., Lo, J., He, Y., Liu, F., Eun, A., Wen, Z.
and Peng, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 30-MAY-2002
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniform;
, Cyprinidae; banio.
1 (bases 1 to 522)
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HS01B22T HS Hordeum vulgare subsp. vulgare cDNA clone HS01B22
                                                                                                                                     15,000 unique zebrafish EST clusters from two cDNA libraries Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensert: 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC
                                                                                                                                                                                           Contact: Peng J
Lab of Functional Genomics
Lab of Functional Genomics
30 Medical Drive, Singapore, 117609, Singapore
Email: penglirabinch.a-star.edu.sg
Clone requests: penglirabincho.a-star.edu.sg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or fish"
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Pred. No. 5e+02;
0; Mismatches 13;
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/cultivar="barke"
/db xref="taxon:112509"
/clone="HS01B22"
/tissue_type="embryo + scutellum"
                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/mol_type="mRNA"
/strain="local wildtype"
/db_xref="taxon:7955"
/clone="159-C11-2"
/tissue_type="whole embryo on /dev_stage="mixed stages"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: stein@ipk-gatersleben.de
Insert Length: 627 Std Error:
Plate: 1 row: B column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="PJR-Z1+Z2"
148 c 117 g
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BQ466638
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Best Local Similarity 72.3%;
Matches 34; Conservative
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  Danio rerio
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BQ466638
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/organism="Hordeum vulgare subsp. vulgare"
/mol types="MRNA"
/cultivar="barke"
/dultivar="barke"
/dultivar="barke"
/dultivar="barke"
/db_xref="cABI:344104"
/db_xref="cABI:344104"
/db_xref="cABI:344104"
/db_xref="cABI:344104"
/dev_srage="con:112509"
/clone="HSO7A16"
/dev_srage="con:12509"
/clone="type="embryo + scutellum"
/dev_srage="0.16 hours after imbibition"
/dev_srage="vector: pBluescript SK+; Site_I: EcoRI (5'-end of cONA); Site_2: XhoI (3'-end of cONA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, Pstl). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable."
                                                                                                                         ע אפאנין אואה א 156 bp mRNA linear EST 23-APR-2003
HSD/A16u HS Hordeum vulgare subsp. vulgare cDNA clone HSD/A16
3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                          Hordeum vulgare subsp. vulgare
Hordeum vulgare subsps. vulgare
Hordeum vulgare subsps. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
1 (bases 1 to 456)
Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
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0
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387 TGCCGTTCTCGTTCGCTCTCGTGGTCGCCGCGGCCGCGCTCTCC 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: stein@ipk-gatersleben.de
Insert Lenghr: 456 Std Brror: 0.00
Plate: 7 row: A column: 16
Seg primer: M13uni.
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AL925722 AL925722
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Danio rerio (zebrafish)
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KEYWORDS
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AL925722
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Best Local
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/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
/lab_host="Wector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG035039 1145 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-010302.F, genomic survey sequence.
AG035039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                       Gaps
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Unpublished
2 (bases 1 to 1145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                Score 26.2; DB 13; Length 627;
Pred. No. 5.2e+02;
0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
173 c 530 g 24 t 72 others
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Pred. No. 5.7e+02;
0; Mismatches 10;
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-010J02.F"
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                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 72.3
Matches 34; Conservative
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Best Local Similarity 75.6
Matches 31; Conservative
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R.Site 2
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AG035039/c
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CB680101
OSJNEf04G16.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf04G16 5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases I to 885)
Jantasuriyarat, C., Lu, Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Largee-scale identification of ESTs involved in the interaction
Unpublished
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="OSJNEf04G16"
/tissue_type="Leaf"
/dev stage="leaf"
/dev stage="l
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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9 CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAG 50
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ilarity 76.2%; Pred. No. 6.2e+02;
Conservative 0; Mismatches 10
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BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: G column: 16
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I basea 1 to 1057)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lissue_type="retina"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for Eull-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
179 c 267 g 253 t 20 thers
                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM14044 row: b column: 15

High quality sequence stop: 397.
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1006107G12.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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/cultivar="mixed background W23/A188/B73"
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Fax: 650 725 8221
Email: walbocderanford.edu Plate: transposon-tagged.
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           1. 1057
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491918"
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Walbot, V.
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BH222532
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Matches 35; Conserv
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/dlone liba="look - RescueMu Grid G"
/dlone liba="look - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamH1; Site 2: Bg1II;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb iastate.edu' and follow the links for
'RescueMu. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and Bg1II, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, 2ea.
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Citek
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA 121: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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Class: sheared ends.
Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                          171 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU667306 478 bp mRNA linear EST 30-SEP-2002 U002E04 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone U002E04, mRNA sequence.
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Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Janag, Y.X., Yu, F.C., Gao, O.K. and Lou, Y.C.
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M.grisea"
         Contact: Bruce A. Roe, University of Oklahoma, broegou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma Advanced Center for Genome Technology, University of Oklahoma Tel: 405 325 4912.
Fax: 405 325 7762
Email: broegou.edu
Contact Dr. Marian Beremand regarding clone availability
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Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Roda 168#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86992051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
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                                                                                                                                                                                                                           High quality sequence stop: 114.
Location/Qualifiers
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128 c 146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: htdong@zjuem.zju.edu.cn
Seg primer: M13 forward primer.
Location/Qualifiers
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Oryza sativa
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KB Zea mays genomic clone ZMMBMa0082D20,
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1 (bases 1 to 873)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-888-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                           609 CGCTCGCGCTCTCCTCGCTCGCCGCGCTCCCGGCCTC 645
                       9 CTCTCACGCTCTCATCGCTCTCGTCGCCGCCTC 45
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Fusarium sporotrichioides
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genomic survey sequence.
BZ547241
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BI189998
BI189998.1 GI:14663677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSB: OGAKP22TM
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Class: sheared ends.
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Zea mays
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02-JUN-2000

DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 29

BH411461

Matches

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ORIGIN

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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1..630
| Organism="Homo sapiens" | Anolyte="manna" | Anolyte="manna" | Anolyte="manna" | Adb zref="tanna" | Adolt" | Aclone lib="HN0006" | Aclone lib="HN0006" | Anote="Organ: head normal; Vector: pucl8; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRnA and cDNA amplification were performed under low stringency conditions: "
                                                                                                                                                                          Bukaryotza, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo.

1 (bases i to 630)

1 (bases i to 630)

1 bass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCO-HN0006-160 300-011-h09&t3=2000-03-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence start: 5
High quality sequence stop: 478.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AW984083 630 bp mRNA linear EST 02-JUN-200
RCO-HN0006-160300-011-h09 HN0006 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.2%; Score 25.6; DB 10; Length 630; 70.8%; Pred. No. 7.7e+02; tive 0; Mismatches 14; Indels 0;
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                                                                              AW984083.1 GI:8175681
                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
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/mol_type="genomic DNA"
/dol_type="genomic DNA"
/dol_type="legenomic DNA"
/disue_type="leaf"
/fisue_type="leaf"
/dev stage="adult"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib==1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHf; Site 2: Bg1II;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.amdb.iastate.edu' and follow the links for 'RescueMu' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and Bg1II, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

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1007022G03.x2 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
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                                                Length 478;
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2221
                                                                                                                                                       9 CTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCC
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ن
                                                   DB 13;
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                                                Score 25.6; DB 13
Pred. No. 7.4e+02;
0; Mismatches 9
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/organism="Zea mays"
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Location/Qualifiers
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Plate: 1007022 column: 11
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                                                   49.2%;
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/dev stage="3 week"
/dev stage="3 week"
/lab host="DHIDB"
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/clone_lib="OSJNEC"
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/clone_lib="OSJNEC"
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//note="Weetor: pBluescript II KS +; Site_l: EcoRI; Site_2:
//note="Weetor: pBluescript II KS +; Site_l: EcoRI; Site_2:
//note="Weetor: pBluescript II KS +; Site_1: EcoRI; Site_2:
//note="Weetor: pBluescript II KS +; Site_1: EcoRI; Site_2:
//note="Weetor: pBluescript II KS +; Site_1: EcoRI; Site_2: PBluescript II KS +; Site_2: PBluescript II KS +; Site_3: PBlue
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Rexroad, C.E. and Keele, J.W.
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USDA, ARS, National Center for Cool and Cold Water Aquaculture
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Lectown Road, Kearneysville, WV 25430, USA
Tel: 304 724 0340 x2129
Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Email: crexroad@ncccwa.ars.usda.gov
Email: crexroad@ncccwa.ars.usda.gov
trimmed with the aid of the trim_alt option. Vector identified by Seq primer: AGCGGATAACAATTCACACAGGA.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 773)

Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazuz Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
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BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: H column: 04
Seq primer: gta aaa cga ccg cca gtg.
Location/Qualifiers
1 .73
1 .773
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/aultivar="Nipponbare"
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                                                                                                                                                                                                                                  Unpublished Contact: Now Wing Arizona Grand Mark Arizona Generic Rod Wing Arizona Genemics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ B5721-0088, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu
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Pred. No. 8e+02;
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Oncorhynchus mykiss
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/clone="OSJNEc13H04"
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Matches 31; Conservative (
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 Taiticeae; T to 402)
Tingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
Dupont Wheat cDNA Sequence
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/lab_host="DH10B"
/clone lib="NCCWA IRT"
/note="Voctor: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
a 166 c 131 g 172 t
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/note="Woctor: pBluescript SK+; Site_1: EcoRI; Site_2:
Xho1; Wheat (Triticum aestivum L.) root; normalized_from wrei library"
85 c 106 g 69 t 16 others
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E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 1)714-6104, USA
Fal: 302-631-2602
Fax: 302-631-2602
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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1 Similarity 75.0%; Pred. No. 9.5e+02;
30; Conservative 0; Mismatches 10;
organism="Oncorhynchus mykiss"
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Triticum aestivum
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Ebwaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Englishea; Poaceae; Pooideae; Triticaeae; Triticaeae; Triticaeae; Triticaeae; Triticaea; Triticaea; Triticaea; Triticae; Triticae; Triticae; Tringey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
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/clone="11517_2A"
/clone lib="Rice panicle at flowering stage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wds3f.pk001.fl5 wds3f Triticum aestivum cDNA clone wds3f.pk001.fl5 cA726.NOV-2002
S. end, mRNA sequence.
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/mol_type="mRNA"
/mol_type="mRNA"
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/lab-bot="wds3f"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat 10 day old seedling full length without
Email: teasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
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Pred. No. 1.1e+03;
0; Mismatches 15; Indels
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E. I. Dubont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2602
Fax: 302-631-2607
Fax: 302-641-2607
Seq primer: M13.
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Best Local Similarity 69.4%;
Matches 34; Conservative
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                             wdk3c.pk006.ll6 wdk3c Triticum aestivum cDNA clone wdk3c.pk006.ll6
5' end, mRNA sequence.
                                                                                                                                                               Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 (bases 1 to 522)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,M. and Hanafey,M.K.
DuPont, Wheat cDNA Sequence
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzae, Liliopsida, Poales, Poaceae, Chysae, Oryza, Liliopsida, Toales, Toales, Oryza, Rice cDNA from panicle at flowering stage
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clome_lib="wdk3c"
/note="vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) developing Kernel, 14
days after anthesis."
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 3102-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
/mol_type="mRNA"
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/lab_host="DH10B"
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Crop Genetics
                                                                                                         CA712672
CA712672.1 GI:25434465
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EST.
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
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CA712672
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C72378
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/organism="Hordeum vulgare subsp. vulgare"
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1 Similarity 69.4%;
34; Conservative (
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Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wisidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
i Gases II: Malvales; Malvaceae; Malvoideae; Gossypium.
I (bases II: Malvales; Malvaceae; Malvoideae; Gossypium.
I (bases II: Malvales; Malvaceae; Malvoideae; Gossypium.
I (bases II: Malvales), Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                       AW730728
GA Ea0027103 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA Ea0027103, mRNA sequence.
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Qutob,D., Hraber,P.T., Sobral,B.W.S. and Gijzen,W.
Comparative analysis of expressed sequences in Phytophthora sojae
Plant Physiol. 123 (1), 243-254 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="8400"
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78 c 184 g 72 t
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Phytophthora.
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11-9B-MY PsojaeMY Phytophthora sojae cDNA, mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 449
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Agriculture and Agri-Food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 449.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
                                                                                                                AW730728.1 GI:7628277
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Phytophthora sojae
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Fax: 864 656 4293
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Bukaryorat, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Bukaryorat, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum;

T (bases 1 to 591)

S Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,

Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.

Development of Barley Transcriptome Resources

NL Unpublished

On Jan 10, 2002 this sequence version replaced gi:18113718.

Contact: Waugh R, Marshall DF

Genome Dynamics (Computational Biology

Scottish Crop Research Institute

Truccardia.
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1391 Sandford Street, London, Ontario, Canada NSV 4T3 Tel: 519 457 1470 Fax: 519 457 3997 Email: 9ijzenm@em.agr.ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 10; Length 569;
Pred. No. 1.1e+03;
0; Mismatches 15; Indels
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
Email: equence has a Phred quality score of 20
Seq primer: M13 reverse.
                                                                                                                                        Location/Qualifiers
1. .569
/organism="Phytophthora sojae"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhatroideae; Oryzae; Oryza.
I (bases 1 to 68)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction Unpublished
                                                                                                                                                                                              /note="Vector: pSPORT1; Site_1: Sal 1; Site_2: Not 1; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SERAD funded cereal IGF (Investigating Gene Function) as 248 c. 108 g. 121 t.
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OSJNEb13C08.f OSJNEb Oryza sativa (japonica cultivar-group) cDNA
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XhoI; 24 hrs after innoculation with Rice Blast (Che 86061
                                                                                                                                                       /clone lib="root, 3 week, drought-stressed, cv Optic,
EBro08"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 625 3967
Eax: 520 621 9288
Email: http://genome.arizona.edu
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Matches 34; Conservative
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AF013256 AC105307 AC120087 AC126527 AC091017 AC098566

219080

U39835 Coccidioide U32518 Coccidioide

CIU39835 CIU32518

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CIU51200

SUMMARIES

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003
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AE008035 Agrobacte
AE009069 Agrobacte
AP003543 Oryza sat
AP003569 Oryza sat
AC114896 Oryza sat
AC130601 Oryza sat
AC310601 Oryza sat
AL931802 Oryza sat
AL931802 Oryza sat
AL939129 Streptomy
AE005738 Caulobact
AP228604 Trypanoso

AE005119 Halobacte AE004888 Pseudomon AC026810 Homo sapi AL731580 Oryza sat

AF232003 Pseudomon AF461561 Pseudomon X98916 M.kandleri AE010324 Methanopy

TBBCHR1A2 PSU96179

AF232003 AF461561

MKFWCB AE010324 AE005119 AE004888

10264 14623

AC026810

114354

101237

SC0939129

AE005738

10037 141983 281000

CNS08C87 CNS08CAF

140556 144077 152359 168864 292200

118444

Oryza sat Homo sapi

AC016651

ALIGNMENTS

AC084081 Homo sapi AP005427 Oryza sat AC107959 Homo sapi Y18102 Oryctolagus

AC107959 OCU18102 AE008035 AE009069 AP005454 AP003513 AP003569

6000 10951 11764 106732 139487

LEISERTHRE AC073431 AP005635

AP005637

162208

AC084081

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AP004769 AC140331

AE017063 AF092435

253253 55939 148301 306067 3582 135357 230357 2595 117846 149082

CIU39835 1201 bp mRNA linear PLN 18-JAN-1996 Coccidioides immitis immunoreactive cell wall protein mRNA, Complete cds. U3983S Coccidioides posadasii Coccidioides posadasii Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides. 1 (Bases 1 to 1201) Dugger, K.O., Villareal, K.M., Ngyuen, A., Zimmermann, C.R., Law, J.H. and Galgiani, J.N. U39835.1 GI:1161373

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PSETABPTABPTABPTABPTABPTABPTHEPPEBPTAVPTGTGGGVPTGTGSFTVTGR
PTASTPAEFPGGSNVRASVGGIAAALLGLAAYL"
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Coccidioides immitis antigen 2 protein gene, complete cds.
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Zhu.Y., Yang,C., Magee,D.M. and Cox,R.A.
Zhu.Y., Vang,C., Magee,D.M. and Cox,R.A.
Submitted (12-MAR-1996) Rebecca A. Cox, Clinical Investigation,
Texas Center for Infectious Disease, 2303 S.E. Millitary Dr., San
Antonio, TX 78223, USA
Antonio, TX 1823, USA
Location/Qualifiers
                                                      /note="major T-cell-reactive component of mycelia and spherule cell walls"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioles.
I (bases 1 to 1435)
Zhu,Y., Yang,C., Magee,D.M. and Cox,R.A.
Coccidioles immitis antigen 2: analysis of gene and protein
97128779
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Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  PTASTPAEFPGAGSNVRASVGGIAAALLGLAAYL"
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/mol_type="genomic DNA"
/strain="Silveira"
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/note="21 A nucleotides"
383 c 277 g 322 t
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                                 /gene="Ag2"
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/product="immunoreactive spherule cell wall protein"
/product="immunoreactive spherule cell wall protein"
/product="immunoreactive"
/db.xref="de":Ad4049140".1"
/translation="WQFSHALIALVAAGLASAQLPDIPPCALNCFVEALGNDGCTRLT
DFRCHCSRPELEDGOITPCVEEACPLDARISVSNIVVDGCSKAGVPIDIPPVDTTAAPE
PSETAREPTARPTEEPTARPTARPTARPTARPTABPTHEPPTEEPTAVPTGTGGGVPTGTGSFTVTGR
PTASTPAEFPGAGSNVRASVGGIAAALLGLAAYL"
369 c 275 g 308 t
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2 (bases 1 to 1201)
2 (bases 1 to 1201)
Dugger, K.O. and Galgiani, J.N.
Direct Submission
Submitted (01-NOV-1995) Kris O. Dugger, Infectious Diseases,
Submitted (01-NOV-1995) Kris O. Dugger, Infectious Diseases,
University of Arizona, 1501 N. Campbell, Tucson, AZ 85724, USA
Location/Qualifiers
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Submitted (27-JUL-1995) Texas Center for Infectious Disease,
Research Immunology, 2303 S.E. Military Drive, San Antonio, TX
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Molecular cloning and characterization of Coccidioides immitis
antigen 2 cDNA
Infect. Immun. 64 (7), 2695-2699 (1996)
96294782
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Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
Cloning and sequence analysis of the cDNA for a protein from Coccidioides immitis with immunogenic potential Biochem. Blophys. Res. Commun. 218 (2), 485-489 (1996)
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On Feb 24, 1996 this sequence version replaced gi:1184058.
Location/Qualifiers
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/mol_type="mRNA"
/strain="Silveira"
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.Corganisma="Coccidioides posadasii"
/mol_type="mRNA"
/strain="Silveira"
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Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 52; Conservative 0; Mismatches 0;
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152_.736
/note="33 kDa_apoglycoprotein"
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/cell_type="spherule"
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|/gene="Ag2"
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Rattus norvegicus clone CH230-345D21, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
AC120087.4 GI:23194659
                                                                                                                                                                                                                                            Zhu, H., Lewin, H.A., and Roe, B.A.
Direct Submission
Direct Submission
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **NOTE: This is a "working draft' sequence. It currently consists of a contrigs. Gaps between the contigs are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence will be preserved.

**This sequence will be preserved.

**Jato: contig of 3409 bp in length 3409: contig of 5877 bp in length 3409: contig of 5877 bp in length 3509: gap of unknown length 9487: 19601: contig of 1015 bp in length 9487: 19601: contig of 1015 bp in length 19602: 19701: gap of unknown length 19602: 37767: contig of 17273 bp in length 19602: 37767: contig of 17273 bp in length 55040: contig of 17273 bp in length 55040: contig of 18599 bp in length 19703: 37667: contig of 26599 bp in length 19704: contig of 26599 bp in length 107642: contig of 26599 bp in length 107642: contig of 26599 bp in length 107742: 197059: contig of 28802 bp in length 107742: 197069: contig of 89318 bp in length 107742: 197069: contig of 88318 bp in length 107765.
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/mol_type="genomic DNA"
/db_xref="texon:9913"
/clone="142-407c.20"
/clone=lib="RPCI - 42 Male Bovine BAC Library"
a 60390 c 59374 g 37137 t 701 others
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                     1 (bases 1 to 197059)
Zhu.H., Lewin,H.A. and Roe,B.A.
Bos Taurus BAC Clone rp42-407c20
Unpublished
(bases 1 to 197059)
    Sovidae, Bovinae, Bos
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                                                                                                          AP013256 3821 bp DNA linear PLN 22-AUG-2000 Coccidioides immitis proline rich antigen (PRA) gene, complete cds.
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Bos taurus clone rp42-407c20, WORKING DRAFT SEQUENCE, 8 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peng.T., Orsborn,K.I., Orbach,M.J. and Galgiani,J.N.
Direct Submission
Submitted (09-UU-1997) Infectious Disease, University of Arizona,
1501 N. Campbell, Tucson, AZ 85724, USA
Location/Qualifiers
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                        Peng, T., Orsborn, K.J., Orbach, M.J. and Galgiani, J.N. Proline-rich vaccine candidate antigen of Coccidioides immitis: conservation among isolates and differential expression with spherule maturation
J. Infect. Dis. 179 (2), 518-521 (1999)
                                                                                                                                                                                                                    Coccidioides posadasii
Coccidioides posadasii
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitogoric Onygenales; Coccidioides.
1 (bases 1 to 3821)
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join(896. .976,1055. .1193,1296. .1660)
/gene="PRA"
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/gene="PRA"
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/organism="Coccidioides posadasii"
/mol rype="genomic DNA"
/mol rype="genomic DNA"
/db xrei="taxon:199106"
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100.0%; Pred. No. 3.2e-05;
ive 0; Mismatches 0;
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/protein_id="AAB66894.1"
/db_xref="GI:2331289"
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ACI05307.12 GI:27764694
HTG; HTGS_PHASE2; HTGS_DRAFT.
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ACLIABS 77 253253 bp DNA linear HTG 13-MAY-2003 Rattus norvegicus clone CH230-157M5, WORKING DRAFT SEQUENCE, 3 UNDOCHERED pieces.
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* NOTE: This is a "working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fauture table below represents a scaffold in the Atilas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs with the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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56238 a 44171 c 42521 g 57422 t 18728 others
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM

    .219080
    /organism="Rattus norvegicus"

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/db_xref="taxon:10116"
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21153. .22325
/note="wgs_contig"
22827. .24533
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                                                                                           Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus nozvegicus (Norway rat)
Rattus norvegicus
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Rat Genome Sequencing Consortium.
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Tallen, C. Allen, H. Alabrooks, S. Amin, A. Angulano, D. Allen, C. Allen, H. Alabrooks, S. Amin, A. Angulano, D. Anyalebechi, V. Avogai, A. A. Avodeji, M. Baca, E. Baden, H. Balden, D. Bandaranike, D. Barber M. Baca, E. Baden, H. Baldvin, D. Bandaranike, D. Barber M. Barsteed, M. Benahmed, F. Biswalo, K. Bladt, T. S. Bankenburg, K. Blyth, P. Brown, M. Baryart, M. Buhay, C. Burch, P. Burrell, K. Chen, S. Chu, J. Ceresari, H. Cenner, A. Craver, D. Chev, D. Cheve, D. Chev, D. Chev, D. Chev, D. Chev, D. Chev, D. Chev, D. Cheve, D. Chev, D. Chev, D. Chev, D. Chev, D. Deramo, C. Cockreal, D. Chev, D. Deramo, C. Ding, Y. Dinh, H. Divya, K. Deramo, C. Cockreal, D. Deramo, C. Ding, V. Dinh, H. Divya, K. Deramo, C. Ding, Y. Dinh, H. Divya, K. Chev, D. Deramo, C. Ding, V. Dinh, M. Divya, K. Chev, D. Deramo, C. Ding, V. Dinh, H. Divya, K. Chev, C. Corles, D. Chev, D. Deramo, C. Ding, V. Dinh, M. Divya, K. Chev, C. Corles, D. Chev, C. Corles, D. Deramo, C. Ding, V. Dinh, H. Divya, K. Chev, C. Corles, D. Chev, C. Corles, D. Deramo, C. Corles, D. Chev, C. Corles, D. Dinh, A. Garner, T. Garza, M. Gabregocrgis, E. Ceer, K. Glill, R. Grady, M. Garra, W. Gebregocrgis, E. Ceer, K. Glill, R. Grady, M. Garra, M. Gebregocrgis, E. Ceer, K. Hines, S. Hlayes, A. Henderson, N. Hermandez, R. Hines, S. Hlayes, A. Henderson, N. Hermandez, M. Havels, S. Kelly, S. Man, J. Levan, J. Levan, J. Levan, J. Levan, J. Luty, J. Liu, M. Liu, Y. London, P. Longon, R. Johnson, R. Mangum, B. Mapuad, L. Loubseyed, H. Lozado, R. J. Lu, X. Ma, J. Ma, J. Mangum, B. Mandum, M. Morris, K. Morris, S. McLeod, M. P. Morris, K. Morris, S. Morleod, M. P. Morris, S. Morleod, A. Soderstem, E. Perez, A. Perez, L. Pankor, D. Walder, Murgh, J. Walker, M. Walder, B. Wall, M. Walder, M. Savert, S. Pata, S. Wall, S. Wall, S. Wall, S. Wall, S. Wall, M. Wall, M. Wal
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Baylor Plaza, Houselon, TX 77030, USA

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 253253)
Rat Genome Sequencing Consortium.
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
individual sequence contigs are ordered and oriented, and separated
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                                                                              sequences and whole genome
    by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads will be indicated in the feature table.
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250804: gap of unknown length
35 251997: contig of 1193 bp in length
8 252097: gap of unknown length
8 253253: contig of 1156 bp in length.
Location/Qualifiers
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75.6%; Pred. No. 3e+02;
ive 0; Mismatches 11; Indels
                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-157MS"
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/note="clone_boundary
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  ACUSIO17 55939 bp DNA linear HTG 24-MAR-2001
HOMO SAPIENS CHICOMOSOME 17 CLONE RP11-64A4 map 17, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This record contains 67 individual
contigs. Runs of N are used to been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L11979
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
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Web site: http://www-seq.wi.mit.edu
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AC091017 1 GI:13443169
HTG; HTGS_PHASE0.
Homo sapiens (human)
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PLN 14-FEB-2002

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Unictor submitted (12-FEB-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

S (bases 1 to 148301)

S Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T., Saski, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Sun, S. Daffect Submission

Lorect Submission

Loudited (14-FEB-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

On Jan 29, 2002 this sequence version replaced gi:16554329.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. The following are single sub-clone areas: 1616-1640, 13395-13416, 49634-49704, 67439-67512, and 67613-67642. There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(266. .315,745. .930,1296. .1551,1621. .2295))
/gene="OSJNBa0051J07.1"
                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
    ACO98566 148301 bp DNA linear PLN 14-FEB-200
Oryza sativa chromosome 10 clone OSJNBa0051J07, complete sequence.
ACO98566
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-JAN-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA (bases 1 to 148301)
Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T., Saski,C., Henry,D., Oates,R., Simmons,J., Thurmond,S.K. and Sun,S. Direct Submission
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/gene="OSJNBa0051J07.1"
/note="Contains similarity to wall-associated protein
                                                                                                                                                                                                                                                  Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T., Saski, C., Henry, D., Oates, R. and Simmons, J. Direct Submission
Submitted (24-OCT-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA (bases 1 to 148301)
                                                                                                                                                                                                                                                                                                                                       Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R. and Simmons,J.
                                                                                                                                                             1 (bases 1 to 148301)
Wing R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
Saski,C., Henry,D., Oates,R. and Simmons,J.
Rice Genomic Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
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of 742 bp in length
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of 740 bp in length
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of 748 bp
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of 672 bp
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of 723 bp i
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// Organism="Homo sapiens"
// mol_type="genomic DNA"
// db_xref="taxon:9606"
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Matches 34; Conserv
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GNISIPPEGTKQSSCFLPGFEVTCNDTFSPPRLFLGNSNPGGRQNYGEFEERYYLTT
EEGMPTHLANDDFLFMELMSINLTECVARAYGPVSSDCSLNDTYHLVKRQMTGLAGPF
LISTRNALTAYGWNMEANLARSVRGSCFLKTTGVRLGQPEFATNGSCLGGGCCGGCEIT
GGIGSIAKDMYNFTSPDLYSDNFSKKYPKGYPLVIDFAIRDGFCPAAGQAPPANYACV
SSNSSCVNVTNGDGYICNCSKGYDGNPYIPNGCHDIDEALADSHPELRVLYPCSRNG
ICMNRPGGYDCPCKRGMSGDGKAGTCSEKFPLQAKIVVGDVRVKDKWDEVENTE" /codon_start=1 /product="Putative wall-associated protein kinase" /protein_id="AaL/7114.1" /db_xref="GI:\B652480" /translation="MLMILPCRLLLRLVLATLILAASTDQHVATLPPITLPGCIDKC

RESULT 9 AC098566

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join(39770. .39860,40240. .40335,40997. .41179,41838. .42862)
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                                                                                          SATRNVLLGVGGSVRARIDGVMSGTNYSAACNSLFDTPAKAENGTCMGLGCCEAELAP
ELGMITVSMYKQSNSMWETFPCTYAMVVERSWYNFSLODLYGYDVLDKKFPGGVPLVL
DFAIRNESCPAEGKPLPTACRSSNSLCVNTTNGQGYVCKCQEGYEGNPYLPDGCQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MEGNGTPPFFSQFSSDPGSSAAGFNLSSAAGFYGGSSCSMLAML
FIQENSRAGCAGTMEGEADIDECELRDEQPALRDQYRCYGICKNTIGGYDCQCKFGTK
GDAKTGTCTQLFPLPAMVATLGIIGLTSIVVVVVLFKLLFDERRKTKEFFIKNGGPVL
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TNEI I I QSKVI HKNI I KLIGCCLEVDVPMLVYEFVPRGSLHJI LHGRRKESLPLOKRL
NIAAGAAEGLAYMHSKTSTTI LHGDI KPGNI ILLDENPOPKI SDFGI SRLIA I DKTHTK
TYLOSGLITKQSDV SFGVVLLELLTROKASGEDTRLVTFLDAYT
EDHKGAI DLPRREI LEGGTEVFNNLAI LVVDCLKFEVERRPEMTDVEERLQTMKRSY
VPKSI SDASSSI DT"
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LVTRAQGPVFVSAFQPLCMIITSVLDSTILREDITLGSVIGAVIIAVGLYALIWG"
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PYSPESNGIAEINEADKCVYYRYGGGEGVILYLYVVDDILIVGTNFEVINEVKSFLSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="OSJNBa0051J07.7"
/note="Contains similarity to wall-associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Putative wall-associated protein kinase"
/protein_id="AAL77120.1"
/db_xref="G1:18652486"
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join(45047. .45139,45236. .45387,45474. .45528)
/gene="OSJNBa0051307.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Contains similarity to polyprotein"
join(55288. .55293,56061. .56220,57182. .57537)
/gene="OSJNBa0051J07.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 8; Length 148301;
5.3e+02;
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/product="butative nodulin protein"
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/db_xref="G1:18652487"
join(35194. .36187,36296. .36318)
/gene="OSJNBa0051J07.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Putative polyprotein"
/protein_id="AAL77122.1"
/db_xref="G1:18652488"
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Pred. No. 5.3e
0; Mismatches
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                                                                   /codon start=1
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|oin(29124. .29317,29445. .29576,29765. .29840,30066. .30449)
|gene="OSJNBa0051J07.4"
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DRISENTSFYGQCVEPHPEAFYSGSEEPSFAKPETEPSTCSGLTKESSLKPSPDSKDI
ORIGENFRDDPHSDYEKT"
/note="Contains similarity to Athila retroelement ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein"
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GMHTVKETEMLTTKLDLLVKKLDNQEKGKPQAAVKALDSHITCEVCGNTGHMGNDYPE
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/product=#ypothetical_protein"
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/db_xref="G1:18652
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GVGARAVVAVPKLSAGGEGAKRRSLRTVKSASRAASEAHVAAF"
                                                                                                                                                                                                                                                     'note="Contains similarity to Athila retroelement ORF1
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/note="Contains similarity to wall-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(26603. .26741)
/note="Similar to Stowaway type MITE element"
29124. .30449
                              note="Similar to Tourist_Ol1 MITE element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (32525. .32675)
                                                                                                                                                          'note="Simple Sequence Repeat (AGAT)n"
12889. .13728
                                                                                              note="Simple Sequence Repeat (TA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18054. 18073
/note="Simple Sequence Repeat (TA)n"
18680. 19432
/gene="OSJNBa0051J07.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notes"Hypothetical protein"
join(18680. 18778,19007. 19432)
gene="OSJNBa0051J07.3"
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join(31823. 32131,32929. 32958)
gene="OSJNBaOO51J07.5"
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gene="OSJNBa0051J07.2"
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18054. .1
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L. Submitted (165-MAY-2003) The Institute for Genomic Research, 9712

Submitted (165-MAY-2003) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a contigous sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs, searches of the complete sequence against a peptide database and EST databases. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding RNNAs are predicted by tRNAscan-SE (Sean Eddy,

Location/Qualifiers
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in this region was derived from BAC clone OSJNBa0061H20
(GB:AC113337)."
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GLDERCIKPAQCHPSAS"
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Oryza sativa (japonica cultivar-group)
Sukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/locus tag="OSJNBa0061H20.9"
/note="Similar to RETROTRANSPOSABLE ELEMENT TF2 155 KDA
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                                                                                                                                                                            The Rice Chromosome 10 Sequencing Consortium In-depth view of structure, activity, and evolution of rice chromosome 10
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3288. .3647
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join(8040
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                     2 (bases 1 to 3582)
Carlile, A., Balley, A., Cooper, R. and Clarkson, J.
Direct Submission
Submitted (16-5EP-1998) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS41 9AF, United Kingdom
Location/Qualifiers
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0017C12
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69.2%; Pred. No. 8.4e+02;
tive 0; Mismatches 16; Indels 0
    during infection by Stagonospora nodorum
Mol. Plant Microbe Interact. 13 (5), 538-550 (2000)
20255037
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2 (bases 1 to 135357)
Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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HTG; HTGS_PHASE2.
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36; Conservative
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Complement (join(<46990. .47063,47139. .>47628))

/locus_tag="OSJNBa0061H20.13"

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/codon_start=1

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/cranslation="WRNHSVDLGSFCASOPPERDHANDALEHAPERRRFDIVVDRPF

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PLEDSSRIHHLHNUTNILDDHANQVLELFEPSPFPRGGALPSNRSNGSRCYPSFGDFF

LOLVYAHVYLPLITIGATPMSPSOEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(5<u>5</u>583. .55736,56130. .56253,56590. .56654,57014. .57051,
57776. .57855,58053. .58197,58489. .58621,58778. .58990,
59410. .59488,59804. .60854,60932. .61306,61323. .61773,
                                                                                                       .42427,42908. .>43138))
GASPWAVAAVLVLASHKPSFQMFRPPWHYK"

complement (<40948. .>43138)

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/note="hypothetical protein"

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complement (join (40948. .41069, 42322. .42427, 42908. .43138))

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APPSSEEGIKJIKJIKCISKFNNPRRGVSIAKAQHNVSYGCNQIVNVSPKS"
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Phaeosphaeria nodorum trypsin-like protease (snpl) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1582)
Carllie, A.J., Bindschedler, L.V., Bailey, A.M., Bowyer, P.,
Clarkson, J. M. and Cooper, R.M.
Characterization of SNP1, a cell wall-degrading trypsin, produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                          complement (<46990. .>47628)
/locus tag="OSJNBa0066H20.13"
/note="Similar to (AP003853) zetal COP like protein
(Oryza sativa) E value 2e 30 Identities 75 215 (of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes,
Pleosporales, Phaeosphaeriaceae, Phaeosphaeria.
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Pred. No. 5e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               complement (<46990.
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AF092435.1 GI:3661611
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71.4%;
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Phaeosphaeria nodorum
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Matches 35; Conserv
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LOCUS
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ORIGIN

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us-10-081-935-1.rge

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LEISERTHRE 27-SEP-1993 Leishmania chagasi (clone Cl) protein phosphatase-2C gene, complete
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                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burns, J.M. Jr., Parsons, M., Rosman, D.E. and Reed, S.G. Molecular cloning and characterization of a 42-kDa protein phosphatase of Leishmania chagasi J. Bhol. Chem. 268 (23), 17155-17161 (1993)
         not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 50.4%; Score 26.2; DB 2; Length 230357;
1 Similarity 79.5%; Pred. No. 6.7e+02;
31; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L15559.1 GI:293067
protein phosphatase-2C; serine/threonine phosphatase.
Leishmania donovani
Leishmania donovani
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                 1255: contig of 1255 bp in length
1155: gap of unknown length
21952: contig of 20597 bp in length
22052: gap of unknown length
52073: contig of 30421 bp in length
52773: gap of unknown length
95211: gap of unknown length
95211: gap of unknown length
135051: contig of 19840 bp in length
135151: gap of unknown length
135151: gap of unknown length
17010: gap of unknown length
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95212. .135051

/note="assembly_name:Contig35"

135152. .170910

/note="assembly_name:Contig36"

171011. .230357

/note="assembly_name:Contig37"

a 50684 c 50723 g 65054 t 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22053. .52473
/note="assembly_name:Contig33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-406J20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1356. .21952
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1 (bases 1 to 2595)
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Best Local Similarity
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1356
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LEISERTHRE
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DEFINITION
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are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

• NOTE: This is a 'working draft' sequence.

• This sequence will be replaced

• by the finished sequence as soon as it is available and the accession number will be preserved.

• Location/Qualifiers
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Direct Submission
Submitted (23-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230357 bp DNA linear HTG 23-F:
Mus musculus chromosome UNK clone RP23-406J20, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/culfivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                        Length 135357;
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Sequencing vector: M13; 04
Sequencing vector: plasmid; 1004
Chemistry: Dye-primer ET: 04 of reads
Chemistry: Dye-terminator Big Dye; 1004 of reads
Chemistry: Dye-terminator Big Dye; 1004 of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 230223 bases at least Q40
Consenus quality: 230223 bases at least Q20
Insert size: 196000; agarose-fp
Insert size: 244718; sum-of-contigs
Quality coverage: 17.67 in Q20 bases; sum-of-contigs
Quality coverage: 11.05 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC Web site.http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 26.2; DB 2
Pred. No. 7e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                               /clone="P0017C12"
28659 c 29003 g 39973
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MCPherson, J.D. and Materston, R.H.
The sequence of Mus musculus clone
Unpublished
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Matches 34; Conservative
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ORGANISM
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AUTHORS
TITLE
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AUTHORS
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COMMENT

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Gaps

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Longished Only in Database (2002)

Sasaki, T., Matsumoto, T. and Katayose, Y.

Sasaki, Matsumoto, T. and Katayose, Y.

Direct Submission

Submitted (07-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 30-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tal:81-298-389-746)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

irce

1. .149082
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*** SEQUENCING IN PROGRESS ***.
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HTG; HTGS.2 PHASES.
OTYZA SALÍVA (Japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
clone:P0646C08
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                         1 81715: contig of 81715 bp in length 82745: gap of unknown length 82745: contig of 16149 bp in length 99829: contig of 16149 bp in length 9924 106719: contig of 6796 bp in length 7720 107748: gap of unknown length 1720 107748: gap of unknown length 8855 11554: contig of 5057 bp in length 8855 11554: contig of 1720 bp in length 1846: contig of 1720 bp in length 17846: contig of 1720 bp in length 17846: contig of 1720 bp in length 17846: contig of 1263 bp in length 17846: contig of 1263 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GS1-146A9"
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Submitted (17-JUN-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
On Jul 12, 2001 this sequence version replaced gi:14421582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGRVENNRYDGSLAVSRAFGDREYKLGSGSQLEQKYIALADVQHKDFTFDSNDFYLL
CCGOFVEGDREPNEEVVAYVKQQLETCKNDLAEVKRAKUEEBA IERGSRDN SCMIYOPKD
GSDYAAEPHTTVYPGPFSAPRNSGFRKAYESMADKGWTTVGALLERRYDTLKAABALT
PEETEELSQFENGPEAKLTGAERQKWFSNYFOKLCEAASNGFSDQMERLOSLQQQAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC073431
Homo sapiens chromosome B clone GS1-146A9, WORKING DRAFT SEQUENCE,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 117846)
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                                                                                                                                                                                                              891. .2111
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/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA 49
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891.211
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Scor. 76.2%; Pred. No. 1...
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Unpublished
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Center clone name: GS1-146A9
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                    Location/Qualifiers
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797 c 68
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McCombie, W.R.
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Best Local Similarity 76.2
Matches 32; Conservative
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bede, F., Boguslavkiy, L., Boukhgalter, B., Eronn, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dokkellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreirs, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Crand-Pierre, N., Diaz, J.S., Margais, S., Ginde, S., Goyette, M., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, G., McCarthy, M., McCarthy, M., McCarthy, T., Margais, N., Margais, N., Margais, N., Margais, J., Murphy, T., Maylor, J., Norman, C. H., O'Connor, T., Morthman, D., O'Rell, D., Ollvar, T., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Voung, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Wilson, B., Wu, X., Waman, D., Ye, W. J., Young, G., Zainoun, J., Wilson, B., Wu, X., Waman, D., Ye, W. J., Young, G., Zainoun, J., Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome Research Center Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171665)
                                                                                                                        AC084081
Homo sapiens chromosome 8 clone RP11-89M8 map 8, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
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Web site: http://www.seq.wi.mit.edu
Conteact: sequence submissions@genome.wi.mit.edu
Conteact: sequence submissions@genome.wi.mit.edu
Conteact: sequence submissions@genome.wi.mit.edu
Center project name: L11307
Center clone name: B1307
Center clone name: B1307
Center clone name: B2M M B

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 168994 bases at least Q40
Consensus quality: 168991 bases at least Q20
Consensus quality: 16991 bases at least Q20
Consensus quality: 16991 bases at least Q20
Consensus quality: 169921 bases at least Q20
Consensus quality: 16900; agarose-fp
Insert size: 169000; agarose-fp
Insert size: 169000; agarose-fp
Unsert size: 169000; agarose-fp
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                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens (human)
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                                                      RESULT 18
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Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Published Only in Database (2002)
2 (Bases I to 162208)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (07-AUG-2002) Takuji Sasaki, National Institute of
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/mol type="genomic DNA"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
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/db_xref="taxon:39947"
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

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Local Similarity 76.2%; Pred. No. 7.9e+02;
Net 32; Conservative 0; Mismatches 10; Indels
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Pred. No. 7.9e+02;
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Concervotable only in Database (2002)

E Sasaki, T., Matsumoto, T. and Katayose, Y.

S Sasaki, T., Matsumoto, T. and Katayose, Y.

Direct Submission

Submitted (12-JUN-2002) Takuji Sasaki, National Institute of Submitted (12-JUN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai (2-1-2, Takuba, 1baraki, 130-8602, Japan (E-mail: tsasakianias affro.go.jp, URL:http://rgp.dna.affro.go.jp/, Tel:81-298-38-7441, Fax:81-298-18-7468)

NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Homo sapiens chromosome 8, clone RP11-875011, complete sequence.
AC107959
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
                           Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
clone:P0684H11
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-875011
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Pred. No. 7.8e+02;
0; Mismatches 10
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Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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of 8647 bp in length
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of 439 bp in length
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1. .439
/note="assembly_fragment
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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/note="assembly_fragment"
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168570. .171665
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/clone="RP11-89M8"
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clone lib="RPCI-11 Human Male BAC"
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3835. .1394^^
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5318. .15410
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16172. .16240
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complement (6089, .6395)
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/rpt_family="Aluy"
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/rpt_family="AluSq"
4788. .4944
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397. .6885
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/rpt_family="MIR"
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/rpt_family="MIR"
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11012. .11315
/rot_family="Alusx"
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/rpt_family="LTR36"
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rpt_family="L1M4"
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1. Submitted (14-3M-2002) Whitehead Institute/MIT Center for Genome Research, 310 Charles Street, Cambridge, MA 02141, USA

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Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schubback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, U., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M.
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/db_xref="taxon:9606"
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Hinkle, G., Slater, S.C. and Goodner, B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
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ggrobacterium tumefaciens str. C58 (Cereon)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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/db_xref="SPTREMBL:097791"
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The NH2 terminus of titin spans the Z-disc: its interaction with a novel 19-kD ligand (T-cap) is required for sarcomeric integrity 99034591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-SEP-1998) S. Labeit, EMBL Heidelberg, Meyerhofstr. 1, 69117 Heidelberg, FRG
Related sequences U28657, D83390, X90568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAM 08-AUG-2001
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Litin; titin gene.
Oryctolagus cuniculus
Oryctolagus cuniculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24135 ATGGAGTTCTCTGAACCTCTGCTGGCTCTGAGGGCTGCCTGACTCTCGAG 24184
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70.0%; Pred. No. 7.7e+02;
ive 0; Mismatches 15; Indels
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complement (18764. .18965)
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complement (20255. .20878)
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complement(19349. .19654)
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19655. .19695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MSTA"
complement(19696.
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1. .6000
/gene="titin"
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Labeit, S.
Direct Submission
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Best Local Similarity 70.0°
Matches 35, Conservative
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VERSION
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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SOURCE
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FKKTAGDEBAAPQFIQFSDHTIAPKKAGHYHLYWGNDRKALMDEVTNWPTYPFLMDGA
DIVEEMAAH"
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complement (5758. .6579)

/gene="AGR C 1937"

/note="HYPOTHERICAL 30.9 KDA PROTEIN IN SBM-FBA INTERGENIC
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GLGNMMSSAQSOFNVPLVFAGLLMLAVEGIAMYAVMAMLEKRMTGWAHRSTMGQ"
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/gene="AGK C 1935"
/note="HYPOTHETICAL 28.9 KD PROTEIN IN AADK-SIGZ
/note="HYPOTHETICAL 28.9 KD PROTEIN IN AADK-SIGZ
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complement (7172. .7852)
/gene="AGR C 1942"
/note="HYPOTHETICAL 21.6 KD PROTEIN IN AHCY-HVRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6557. .7175)
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complement (7798. .8646)
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complement (4897. .5580)
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/codon_start=1
/transl_table=11
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/transl_table=
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342. .4030
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ELLMLDEPFGALDAFTREELWVYTRDLHAAGRYTIILYTHDLREATFLADKIFVWSAR

    10951
    Agrobacterium tumefaciens str. C58 (Cereon)

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note="probable permease of ABC transporter PA3512
(imported) - Pseudomonas aeruginosa (strain PAO1)"
Hinkle, G., Slater, S.C. and Goodner, B.
Direct Submission
Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="AGR C 1928"
/note="(AP001514) BH2174
unknown conserved protein in B. subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                complement (97. .1656)
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complement (97. .1656)
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                                                                                                                                                                                Location/Qualifiers
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4027. '.4845
                                                                                                                                                                                                                    .10951
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SAIELERLNMANSYNIKTPYVVENGMGGVDPARLAASLDTLKVSMGLKGNVKAEQVFD
AAYLPPPREERMLP"
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ELLMLDEPFGALDAFTREELWCVIRDLHAAQRVTIILVTHDLREATFLADKIFWMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA 98195-7242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="Atu1047"
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S Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
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The genome of the natural genetic engineer Agrobacterium
tumefaciens CS8
L Science 294 (5550), 2317-2323 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESEPQAONGEOPOQAQPAEPDEVEDESDESDEJDELDERAGRANDQOSAKDTTPENS
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Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9551. .9808)
gene="AGR_C_1947"
note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Matches 34; Conserv
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2 (bases 1 to 106732)
Sasaki,T., Matsumoco,T. and Katayose,Y.
Sasaki,T., Matsumoco,T. and Katayose,Y.
Submitted (20-JUN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai C-1-2, Tsukuba, Ibaraki 305-8602, Japan Research Program; Kannondai (B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:1-298-38-741, Fax:81-299-38-7468)
On Apr 11, 2003 this sequence version replaced gi:21624006.
The orientation of the sequence is from SP6 to T7 of the PAC clone. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7, PAC clone:P0455F03, complete sequence.
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aminomethyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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complement(6998. .7765)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
/transl_table=
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BIVEDRAAAHPQFIQFSDHTIAPKKAGHYHLYWGNDRKALMDEVTNWPTYYPFLMDGA
DIVEDRAAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon start=1
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AGLAYGLALQGTLOVANAAAADATAGFRAGESTIETSTYSTSILLD
PAPVTFVDSYTADSATVKLRYWYRSDNYFVTTRDVTKAMRLAFDERKAEVNAQPA"
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DGNVPFVLPLAG"
TIEPETEDVLRALGAKKADIMLKVGIPRSMPYFFGSLKIAITLAFVGSVVSETVASNY
GLGNMMSSAQSQFNVPLVFAGLLMLAVEGIAMYAVMAWLEKRWTGWAHRSTMGQ"
complement (3126. .3809)
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NGOTRGDHAFTVAQHCLIVETIFCRMCPGATPDEMQMALLHDAPEYVIGDMISPFKSV
VGGGYKTVEKRLEAAVHLRFGLPPHASRELKDRI#KADTVAAFFEATELAGFSTAEAQ
KFFGLPRGITRDMFDIIPLPSTEAQRLFIARFEAIETLRVTRTGGAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4886. .5404)
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complement (4886. .5404)
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located using Blastx/Glimmer"
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/gene="Atul052"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon startal
/transI_table=11
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                                                                                                              complement (3126. .3809)
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Ly Submitted (11-APR-2001) Takuji Sasaki, National Institute of Submitted (11-APR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469]

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

• NOTE: This is a "working draft' sequence.

• This sequence will be replaced

• This sequence will be preserved.

• This sequence will be preserved.

• The accession number will be preserved.
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HTG; HTGS PHASE2.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/mol type="genomic DNA"
/cultivar="Nipponbare"
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/chromosome="6"
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Oryza sativa nipponbare(GA3) genomic DNA,
clone:P0690H04
Dublished Only in Database (2001)
Closses 1 to 139487)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                          Score 25.6; DB 8;
Pred. No. 1.1e+03;
0; Mismatches 14;
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                            /clone="P0455F03"
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               /chromosome="
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Best Local Similarity 77.5%;
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Best Local Similarity 70.8%;
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RESULT 26 AP003569/c

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Sasaki, T., Matsumoto, T. and Yamamoto, K.

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Matsumoto, T. and Yamamoto, K.

Burect Submission

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakigabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given, however the sizes of the gaps between them

are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is savailable and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be
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HTG; HTGS PHASEZ.
Oryza satīva (japonica cultivar-group)
SM Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
El (bases 1 to 1844a)
S Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K., Xim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B., Jin, S., Ko, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
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Oryza sativa (japonica cultivar-group) chromosome 6 clone P0425F05,
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Oryza sativa (japonica cultivar-group) chromosome 3 clone
OSJNBa0091B22, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
clone:P0425F05
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/cultivar="Nipponbare"
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NAL Unpublished
NCE 2 (bases 1 to 140556)
10RS 2 (bases 1 to 1405202) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taiwan Section 2, Academia Road, Nankang, Taiwan Section 2, Academia Road, Bankang, Taiwan Section 2, Academia Road, Setwen the condities

**NOTE: This is a "working draft' sequence. It currently consists of 5 consists of 5 consists of 8 consists of 128, and 1
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HTG; HTGS PHASE2.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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48.8%; Score 25.4; DB 2; Length 140556;
Best Local Similarity 68.6%; Pred. No. 1.2e+03;
Matches 35; Conservative 0; Mismatches 16; Indels 0;
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Oryza satīva (japonica cultivar-group)
SM Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
Enthartoideae; Oryzeae; Oryza.
Enthartoideae; Oryzeae; Oryza.
S Chow, T.-Y., Haing, Y.-I. C., Chen, C.-S., Chen, H.-H., Liu, S.-M., Chen, Y.-L., Cheng, S.-J., Chen, H.-C., Chen, S.-K., Chen, T.-R., Chen, T.-R., Chen, H.-C., Chen, B.-V., Hsiao, S.-H., Hang, J.-N., Hsu, C.-H., Hunng, J.-J., Kau, P.-I., Lee, M.-C., Leu, H.-L., Lin, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Vu, C.-Y., Yu, S.-W., Wu, H.-P., and Shaw, J.-P.
                            sativa ssp. japonica cv. Nipponbare OSJNBa0091B22 BAC genomic
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Diffect Submission

Submitted (08-MAY-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

ON MAY 8. 2002 this sequence version replaced gi:19881808.

ONTE: This is a 'working draft' sequence. It currently

consists of 5 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

6088

6187: gap of unknown length

6188

227799: contig of 6087 bp in length

6188

227799: contig of 1652 bp in length

62840

80164

80164

80263: gap of unknown length

80164

97039

97139

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19444: contig of 18775 bp in length
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                                                                                                                                                                                                                Direct Submission
Submitted (13-MAR-2002) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
(bases 1 to 118444)
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1. 118444
1. Coganism="Oryza sativa (japonica cultivar-group)" /mol type="genomic DNA" /cultivar="Nipponbare"
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48.8%; Score 25.4; DB 2;
Best Local Similarity 68.6%; Pred. No. 1.2e+03;
Matches 35; Conservative 0; Mismatches 16;
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L68864 bp

DNA linear HTG 07-MAR-2003

CSJNBABO083D13, *** SEQUENCING IN PROGRESS ***.

AL831802

AL831802

AL831802.4 GI:28892660

SHTG; HTGS PHASE2; HTGS ACTIVEFIN.

Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

ENKARYOCA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enrhartoideae; Oryzae; Oryzae; Oryzae;

Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelletier, E., Scarpelli, C., Salanoubat, M., Order, C., Cattolice, E., Salanoubat, M., Order, C., Cattolice, C., Salanoubat, M., Order, C., Cattolice, C., Cattolice, C., Salanoubat, M., Order, C., Cattolice, C., Cattolice, C., Salanoubat, M., Order, C., Cattolice, C., Cattolice, C., Cattolice, C., Cattolice, C., Cattolice, C., Salanoubat, M., Order, C., Cattolice, C., Cattolice,
                                                                                                                                                                                                                                                  The following sequence is oriented from the T7 to the SP6 end. IMPONTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The mucleotide sequence of this BAC clone was generated by combining Syngente and Genoscope sequencing data.

* NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* I 152159: contig of 152159 bp in length.
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
On Mar 9, 2003 this sequence version replaced gi:28460535. Center: Genoscope / Centre National de Sequencage Center code: GS Web site: http://www.genoscope.cns.fr/Contact: SeqRef@genoscope.cns.fr
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/db_xref="taxon:39947"
/chromosome="12"
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/clone_lib="OSJNBa"
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CHASPERATOR (Japonica cultivar-group)
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AL Submitted (08-MAY-2002) The Institute for Genomic Research, 9712

Submitted (08-MAY-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

On May 8, 2002 this sequence version replaced gi:20146765.

**NOTE: This is a 'working draft' sequence. It currently

**consists of 7 contigs. Gaps between the contigs

**are represented as runs of N. The order of the pieces

**is believed to be correct as given, however the sizes

**of the gaps between them are based on estimates that have

**provided by the submittor.

**This sequence will be preserved.

**This sequence will be preserved.

**Py the finished sequence as soon as it is available and

**by the finished sequence as soon as it is available and

** the accession number will be preserved.

**1286: contig of 21285 bp in length

**58265: S8364: gap of unknown length

**71534: T1633: gap of unknown length

**71534: T1633: gap of unknown length

**71537: T1633: gap of unknown length

**71557: gap of unknown length

**715585: contig of 2217 bp in length

**715597: R8266: contig of 2916 bp in length

**715597: R8266: contig of 19169 bp in length

**715597: R8266: contig of 2916 bp in length

**715597: R8266: contig of 19169 bp in length

**715597: R8266: contig of 19169 bp in length

**715597: R8266: contig of 2916 bp in length

**715597: R8266: contig of 19169 bp in length

**715597: R8266: contig of 19169 bp in length

**715597: R8266: contig of 2916 bp in length

**715597: R8266: gap of unknown length
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="3"
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Oryza sativa (japonica cultivar-group) chromosome 12 clone OSJNBa0029K06, *** SEQUENCING IN PROGRESS ***.
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/yore= SCO(6.22, possible copper oxidase, len: 343 aa;
weakly similar to members of the multicopper oxidase
family e.g. to the N-terminus of SW:COPA PSESM
(EMBL:M1930). COPA, Pseudomonas syringae copper
resistance protein A precursor (609 aa), fasta scores;
opt: 170 z-score: 188.4 E(): 0.0036, 27.34 identity in 205
aa overlap, Also weakly similar to the blood coagulation
factors which are structurally related to the multicopper
oxidases. Similar to the N-terminus of TR:O53858
(EMBL:AL022004) Mycobacterium tuberculosis hypothetical
protein (504 aa) (25.1% identity in 323 aa overlap).
Contains PS00079 Multicopper oxidases signature 1 and
PS00080 Multicopper oxidases signature 2 (the latter
/cadon_statt=1
/transl._table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / L-anslation="MDRRGFREKGRASUPGPLIEVNEGTAPAKGITARTAPA
/ Crasislation="MDRRGFREKGRASUPGPLIEVNEGDTLHIEFTNTMDVRASLH
VGGLDYEISSDGTAANKSDVBEGGTRYTWRTHKPGRRDDGTWREGSAGYWHYHPHVV
GTEHGTGGIRNGLYGPVIVTRKGDVLPDATHTIVFNDWTINNRKPHTGPDFEATVGDR
VGIVWITHGEYYHTFHMGHRWADNRTGILTGPDDPSRVIDNKITGPADSFGFQIIAG
GGYGAGAWMYYHCHVQSHSDMGMYGFLVKKPDGTIPGYEPHEHGGATAKSGESGEPTG
GAAAHEHEH"
                                                                                                                                                                                                                        Direct Submission
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: sdb@sanger.ac.uk
On or before Oct 29, 2002 this sequence version replaced
gi:2052076, gi:2052079, gi:20520672, gi:20520776, gi:20520777,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC0613"
/note="SC466.23, probable lacI-family transcriptional
/note="SC466.23, probable lacI-family transcriptional
regulator, laen: 35.2 as, similar to many e.g. TR:087590
[EMBL.AF08619], CalR, Thermomonospora fusca
transcriptional regulator of cellulase genes (340 aa),
fasta scores; opt: 991 z-score: 1119.2 E(): 0, 51.9$
identity in 324 aa overlap, Similar to others from S.
coelicolor e.g. TR:086795 (EMBL.AL031317) S. coelicolor
putative transcriptional regulator (355 aa) (36.3$
                   Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="repeat 7; 23 bp imperfect inverted repeat"
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/note="PS00079 Multicopper oxidases signature 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="PS00080 Multicopper oxidases signature 2"
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/mol_type="genomic DNA"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative copper oxidase"
/protein_id="CAB45586.1"
/db_xref="G1:5139568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: SC4C6.22"
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1276. .2334
                                          coelicolor A3(2)
Nature 417 (6885), 141-147 (2002)
21996410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:100226"
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/gene="SCO6712"
                                                                                                                                                      2 (bases 1 to 292200)
Bentley, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .292200
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JOURNAL
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                                                                                                                                                                                                 AUTHORS
                                                                        JOURNAL
                                                                                                                                      PUBMED
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             TITLE
                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                             The following sequence is oriented from the T7 to the SP6 end.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences.

The nucleotide sequence of this BAC clone was generated by combining Syngents and Genoscope sequencing data.
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Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Cronin, A., Fraser, A., Golba, A., Hidalgo, J., Hornsby, T., Howarth, S.,
Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neil, S.,
Seeger, K., Saunders, D., Sharp, S., Squares, S.,
Taylor, K., Warren, T., Warzer, S.,
Parkhill, J. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SC0939129 292200 bp DNA linear BCT 11-FEB-Streptomyces coelicolor A3(2) complete genome; segment 26/29. AL939129 AL049485 AL049587 AL079355 AL138598 AL138667 AL138668 AL138977 AL353864 AL353870 AL355693 AL356812 AL645882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is believed to be correct as given, however the pieces of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 168864: contig of 168864 bp in length.
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Bacteria; Actinobacteria; Actinobacterias; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .168864

/organism="Oryza sativa (japonica cultivar-group)"

/mol type="genomic DNA"

/cultivar="Nipponbare"

/sub species="japonica"

/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7885 TGCAGCCCGCTCGCGTTCTTGTTGCTCTCGCCGCAGCCGTTCTTGCTCTTG 7835
On Mar 9, 2003 this sequence version replaced gi:28460587.
Center: Genoscope / Centre National de Sequencage
Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contigs composition:
166717 bp contig from 1 to 166717
2097 bp contig from 166768 to 168864.
• NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs
• are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.8%; Score 25.4; DB 2; Length 168864; 68.6%; Pred. No. 1.2e+03; ive 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGTG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 others
                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="OSJNBa"
45973 a 38589 c 38829 g 45421 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="12"
/clone="OSJNBa0083D13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor A3(2)
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Matches 35; Conservative
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ACCESSION
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ORIGIN
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KEYWORDS
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   COMMENT
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8

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/note="SC4C6.26, hypothetical protein, len: 64 aa; unknown function, probable CDS suggested by positional base preference, GC frame plot and amino acid composition" /codon start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_cable=11
/product="hypothetical protein"
/protein_id="cabs550.1"
/db_xref="G1:5139572"
/translation="MCRAAGGVAAALLTEAAAEPLAVTGALGECEDRPAPWRELPRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCT 12-JUN-2002
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1 (Bases I to 10037)

Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Bisen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Bly, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Shetty, J.F., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ernoleeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                            /trānslation="MHTETTAAPDLSWQEEALCAQTGGDFFFPEPGSSVRDAKRICAL
CPIRSTCLEFALSNDERFGVWGGLSEKERLALRRTIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 10037)
Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J.,
Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I.,
Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /noce="SC4C6.27c, probable acyl-(acyl-carrier protein) desaturase, len: 328 aa; similar to many e.g. Sw.STAD LINUS (EMBL:X70962) Linum usitatissimum stearoyl-ACP desaturase (196 aa), fasta scores; opt: 385 z-score: 46.15 E(): 2.2e-18, 30.2% identity in 311 aa overlap. The N-terminal 100 aa are divergent. Highest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE005738 10-JUN 10037 bp DNA linear BCT 12-JUN Caulobacter crescentus CB15 section 64 of 359 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279401 ATGCGGTACGCCAACGCGGCCGCCCTCGTCGCCTCTCGCCTGT 279351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.8%; Score 25.4; DB 1; Length 292200; 68.6%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCAGT 51
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Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
21173698
                                                                                              /product="putative transcriptional regulator"
/protein_id="CAB45589.1"
/db_xref="G1:5119571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
   identity in 75 aa overlap)"/codon start=1/transT_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: SC4C6.27c"
complement(4242. .5228)
/gene="SCO6717"
                                                                                                                                                                                                                                                                                                                       /note="synonym: SC4C6.26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4242. .5228)
/gene="SCO6717"
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Caulobacter crescentus CB15
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/gene="SCO6716"
                                                                                                                                                                                                                                                         4003. .4197
/gene="SCO6716"
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AE005738/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /noce="SG466.24c, possible hydroxylase, len: 263 aa; similar to TR.055078 (EMBL:U50973) Streptomyces sp. strain C5 daunomycin C-14 hydroxylase (275 aa), fasta scores; opt: 422 z-score: 482.3 E(): 1.5e-19, 38.54 identity in 273 aa overlap. Similar to TR:050527 (EMBL:AL009204) S.coelicolor hypothetical protein (267 aa) (37.94 identity in 253 aa overlap) and to (EMBL:AL049863), SC5HI.09c, S.coelicolor possible hydroxylase (265 aa) (35.74 identity in 258 aa overlap). Also similar to hypothetical proteins from Mycobacterium tuberculosis and to Mycobacterium tuberculosis and to Mycobacterium tuberculosis 27.3 Kba MAb HBT7 reactive antigen (EMBL:AL007737) (260 aa) (36.74 identity in 264 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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AAPPGVVLPTLVHRSTA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="SC4C6.25, probable transcriptional regulator, len:
identity in 342 aa overlap). Contains Pfam matches to entry PF00532 Peripla BP_like, Periplasmic binding proceins and LacI family and to entry PF00356 lacI, Bacterial regulatory proteins, lacI family. Contains probable helix-turn-helix motif at aa 9-30 (Score 2307, +7.04 SD)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF00356 lac1, Bacterial regulatory proteins, lac1 family, score 39.70, E-value
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//note="repeat 7: 23 bp imperfect inverted repeat" complement(2440. 3231)
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SSVIVVSDRNVIDTQLQEALFDFQRTAGVVATIKSESGSKSGQLAEALAAGGKKVIVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQTEPPALEAVREQAATOGKAFAVIANEAHSSOTGEAGKLKOMLSDAEIAELADGGE

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VTAKAQDDERAAAEALLDHMNALDLFKGDMAAFGRLYSFISOTFDRGTERRSIFFR
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complement (7350. .8330)
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                                                                                                                                                               by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="identified by Glimmer2; putative"
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complement(9136. .9471)
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                                                                                                                                                               note="identified
                                                                                                                                                                                                                                            table=11
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Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utcerback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
                                                                                                                                                                                                                                 Genomic Research, 9712
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    10037
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Fraser.C.M.
Procer Submission
Submitted (31-JAN-2001) The Institute for Ger
Submitted (31-JAN-2001) The Institute for Ger
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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FEATURES
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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notes"identified by Glimmer2; putative"
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Pred. No. 1.7e+03;
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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AP003047.2 GI:13122417
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90.0%;
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AUTHOF.S
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RGP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTP2.0. ESTB represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0666G04 clone has an overlap with OJ1174_D05. This sequence of this clone starts at the position 58,198 of OJ1174_D05. This sequence of F066G04 clone has an overlap with P0489A01 (DDBJ: AP002484) clone at the position 119,689 to 141,983 of 3' end. The sequence of this clone ends at the position 19,295 of F0489A01. Detailed information on overlap and assembly quality the profession of this entry is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /crānslation="MQPRRRQQQQSILSFLQKKPAAAAGEEGATPERPPRPAASVA
GIMBRLWPBPRQQQGRDQDASQAHIVEQRALPWRQTTSBEGGSALFLESGNAGDNK
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NNNCIGANSSFEEPVQTQQTSKTVFWRSSRGADTPLTESDSDQTPLQHPSKFSFVS
PNGEYVRGATLFALDSNYTPRRESSEKLSSGPSDLPYIKATKLFTEFDSNGTPSQNHL
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PFWGPNKKVKPAQCSPVENKVHDEMAESARSKFEWLNPSNIRDANRRRLADPLYDKTT
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GSNSVILRKLVHVSTPSTVGDSNIGADAVHLLSLKEITLASNGSRYVGFAFLDYAALK
IWVGSVHDDDTFAALGALLGALLVQVSPKEIIYETSGLSKETHRLIKKYASAGSVKMQLTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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Location/Qualifiers
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Hall,N., Berriman,M., Lennard,N.J., Harris,B.R., Gerrard,C.S., Atkin,R.J. Barron,A.J., Bart-Delabesse,E.N., Bowman,S. Bray-Allen,S.P., Bringaud,F., Clark,L.N., Corton,C.H., Cronin,A., Davies,R., Doggett,J., Fraser,A., Gruter,E., Hall,S., Harper,D.A., Hertz-Fowler,C., Kay,M.P., Leech,V., Mayes,R., Price,C., Quail,M.A., Rabbinowitsch,B., Rucherford,K., Sasse,J., Sharp,S., Showhkeen,R., Gull,K., Barrell,B.G. and Melville,S.E.
The sequence and analysis of the highly polymorphic chromosome I of the African trypanosome, Trypanosome brucei
                                                                                                                     PAVYQALERHLPPDLAGAPAĒVKRYFMRSVLRNYVPSPSORIRTONOREYRERILSAY
QPLHPELYTNDPSTFILPAFLQAINGNTEESITSIMMEPAPGVFAFPMLKPSFCQMLM
SEVNNFLRWAQSANQRIMRPTSLDRHGRGAALSDFGLQEMLDNLMKDFISPMSTVLFP
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complement(join(46556. .46681,51622. .51919,52095. .52141,
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Submitted (20-SEP-2002) The Wellcome Trust Sanger Institute,
Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
For more information about this sequence or the Trypanosoma brucei
broject, see http://www.sanger.ac.uk/Projects/T_brucei. NOTE: This
is the largest contiguous sequence from chromosome I,
spanning between the 70 bp repeat arrays at either end. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berriman, M., Hertz-Fowler, C.V.A., Hall, N., Kerhornou, A.X., Bowman, S., Quall, M., Kay, M.P., Bray-Allen, S., Lennard, N.J., Clark, L.N., Harris, B.R., Melville, S., Gerrard, C., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     size is 1056003 bp but it has been split into 4 database
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TBBCHRIA3 - 478001 . . 478000 (THIS ENTRY)
TBBCHRIA4 - 807001 . . 105603
It replaces the previously submitted unfinished (941631 bp) sequence for T. brucei chromsome I. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                          48.5%; Score 25.2; DB 8; Length 141983; 71.7%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TBBCHR1A2 281000 bp DNA linear Trypanosoma brucei DNA chromosome 1, segment 2/4. AL929604 AL359782 AL929608 AL929604.1 GI:25991392
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complement(1000. .18
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2 (bases 1 to 281000)
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33; Conservative
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                            ò
join(33254. .34423,35296. .35505,35612. .35707,35804. .36025,
36599. .36793,36867. .37013,37093. .37242,37532. .37662,
37748. .37964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0666G04.4"
join(33254. .34423,35296. .35505,35612. .35707,35804. .36025,
36599. .36793,36867. .37013,37093. .37242,37532. .37662,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(42951. .43385,43715. .43762,44108. .44284,44440. .44596,
4728. ...4811,45332. .45387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(42951. .43385,43715. .43762,44108. .44284,44440. .44596,
44728. .44811,45332. .45387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDEMKRGVDISNFRKEKLGSSSNGTIYWYDGDSTIGHRLYSEYYTLDFKRNLKGKNGR
LTKPVINIQWETVATNIDEFYBISEKLCSKGRFBESAIGEHLKTEIIPDVEKLOKKKER
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ESDPQEAGKKERRASHQGNKGANGGSDIGPEQKEDGQEDAGGSDVNPEQDKDGQGEDY
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RTRLASRRPDKPPQCLRRSRNMKNDEDVMRPGQLTPRSMTKKTMRQRPTSISKQFSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / translation="MSVVGFDLGNESCIVAVARQRGIDVVLNEESKRETPAIVCFGDK
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KILSHAVDRSLGGRDPDEVLFKHFAAKKRDEYKIDVYQNARACIRLRYACEKLKKVLS
ANPESPMHIEGLMDEKDVRGFIKREFFEKISASILERVKGPLEKALAEAGLTTENVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVVGSGSRVPAIIKILTDFFGKEPRFTWASECVARGGALECAILSFTFKVREEFOWN DGFPFSIAMSWKPDSQNGDNOQTVVFPKGNPLPSVKALTFYRSNTFQVDVTYVDTGDL OISPKISTYTUGPFNPGKGDKAKLKVKNRLNHIGVVTWESATWLEEEEVSEVPVAATTE PPKDSAWETDDAPNEAASGTDVNMOEAKAPAAADGAENGAPNSEEKSVPWTTDAK VEPSKKKVKTNVMYPNSLVYGALGTTELQKAVEKETSEWALQDRVMESTYDAK VEPSKKKVKTNVMYPNSLVYGALGTTELQKAVEKETSEWALQDRVMESTKOKANESY VYDMRNKLYDKYNDFVTAEDKEAFIAKLQEVEDWLYEDGEDETKGVYNKLEEKKVG GPIEARYKEWMDRGFSIDQLAYCINSFRDAALSKDPREDHIEMEEKQKVINQCSEAEV
                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join(24484. .25102,25464. .25506,25942. .26053,
26232. .26321,26395. .26557,26679. .26785,26919. .27000,
27084. .27121,27204. .27290,28128. .28238,28380. .28517))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similar to Arabidopsis thaliana chromosome 1 F14D16.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein
similar to Arabidopsis thaliana chromosome 3 MRC8.21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETPAGGAQTPEQQPQGAEAAGEASEGGASESTGEQMETDKPEGTEAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="P0666G04.4"
/notce="contains ESTs
D2201(C1025),C26080(C11596),C26176(C11773),
AU085955(EC2104)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0666G04.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0666G04.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37748.
                                                                                                                                                                                                                                                                                                                    gene
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LLHUNRSHTRITELAISSDQSLIATASEDSVCKTWLLAALVARGSAPAPRIYFNGH
SLSVNACSFLDSSQSVVTASSDRSCRIFDGSTGQQFVVTLGDVLTSVRPSPGDEMLL
DYGEFGSLFFVRLYSFSERGCLPTAGLIRCNNDVTCTPFTDGHKGA PFTHPPTTRP
DYGEFGSLFFVRLYSFSERGCLPTAGLIRCNNDVTCTPFTDGHKGA PFTHPPTTRP
OYLUNGSTNGVILWMNIRTATPTEKAVDDIAGGLLSVCYVPSDATQPSSAAVPPVLQ
KHPLDPLGVDFIVVSAGKKESAPISYQKEGGSRASRRKRKHQQTMEDTCVSMKRTENV
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LLRVANVTADDTFFYDLGCGNGSVLFHVALATGGASCVGVEINEHNAKVAKEAWTHLRPV
FEKRRGRKLDVSIVCGDFCKVLKQDNYFSSSCVVWIANLLMPRFVNHYLSERLRSLPI
GSRVLCMEDLYPHSRSVAAARDPDAFEKFEMVDYRWQEDSVEWSPASGPFYLYIKRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Process id="CAB95352.1"

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/translation="MYHPYLWVIIVGGIVSFLTGCGVGMNDLANSFGTTYGSRVLNLW

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FATMMSLPVSSTHSIAGAIIGFALVYGGFGAVSFAKKIDEFPYVTGVAPIIASWFISP

MFAGAVAASLYALLRLVVLRPANSVNRALFALDLIVGCYTFFLESFFVLFKGAKARLHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAKASWVAALIGLGAASISAACIPLLRRRVRLITERAERERAETGMYTAPEISGDAG
AISENAAGVGAAVEGPVDTANRIVPPSSEPTSDSPTAKENPANNASGLTTPGVVDEAL
FRVUJYPERVEYVFRYLQVPTAACASFAHGANDSNAIAPFSAMYSIYINQVVEEN
DVPLWILVLGGAGGLVVGLAYLGVGIMRLLGERITKITPSRGFSAELSVALVVSLCSAF
GIPVSSTHCITGAVVAISIMDCGFRKVRWMNVGKMYLGWIFTLLITAAISALLFAQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNAFGHLCDHOWRKSLRSVVLLPPIFSROLILALSVPYGTVL1I
FFPPPSPFLFFPFFFLCF11PLSCLCSFNLSVLNHTRTAFAPSAAW1PRTLWSHVARR
VALSGGVEGCRVTDVRECLKQN1MLEKVAGSSSSSR"
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and TPB15A20 reads call A, One genomic shotgun read calls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Majority of WCS,TP3D18 and TP7E4;reads call C, Two WCS reads call T, type 1 (single nucleotide substitutions)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Majority of genomic shotgun,TPB15A20,TP3D18,;and
TP7E4 reads call A, Two TP20A12 reads call C
type 1 (single nucleotide substitutions)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10259. .11809)

Ggene="Tb927.1.580"

Complement (10259. .11809)

/gene="Tb927.1.580"

/codon_start=1

/product="phosphate-repressible phosphate permease,
possible="Tb927.1"
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7896
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complement (13430, 13846)
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complement(8396..9223)
/gene="Tb927.1.570"
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RGDIVVDVEYTSRDRSKRICTETNIKIGTIPIMLKSSSCNLYGKGREELIAMRECPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGGYFIIKGVEKVCLVQEQQSKNRVIIEADDNGDIVAHVQSKHHYSISKCSVTFRKGR
IVMVHRSFKEDIPIVVVLKALGMESDQOIAQHIGVSPAFQSVLFACFEHAASLNVKTQ
BDALHFIGERRKETFNEMDETQQRHVQKSKADSAAEFLANULLCHIREGEVQRDWNFR
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AMDQLLSKKOTTKPFNKQVBSKMEVIQNGRNALSSGRWELKFFNMSRQGITQVLS
RLSYISCIGMMTRLASSFEKSRKISGPRSLQPSQWGMVCPCDTPEGESGGLVKNFFIL
SQVTLDMDDSFVRAAAYNLGVEEVDCISPNEFLKYTVFLNGTLMGIHRYPSRLCRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTLRRSGRLHPHYSTAINDROKSVQICCDGGRIVRLYYVRDCKPATSQHLDNLSSG
KCSINDFLAEGLWEFIDWBANDCLIAVYPKDIEDYTHLETEPLSLLGVVAGIIPPP
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RHGYNYHGKDIFYSGVTGEMLAYVFFGPIYYORLICHWYDKHARATGPRSHTTRQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unlikely gene"
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                                                                                                                                                                                                                                                              GNVALRRCDARQLRSLMRSNPLKCAKQHLSVCDDDAAYWLLETVVAVKEYIPLNL"
2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Majority of WCS,TPB15A20,TPB12C6,TP3D18;and TP7E4 reads call C, One WCS read calls T type 1 (single nucleotide substitutions)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note≈"Majority of WCS,TPB15A20,TP3D18 and TPB12C6;reads
                                                                                                                                                                                                                                                                                                                       /noice="Majority of WCS,TPB15A20,TP7E4 and TPB12C6;reads call T, Two TP20A12 reads call C, repp i 1 (single nucleotide substitutions)" /gene="Tb927.1.522. .5611) /gene="Tb927.1.540" /gene="Tb927.1.540" /gene="Tb927.1.540" /gene="Tb927.1.540" /gene="Tb927.1.540"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCNAKNTVSRVNVPYAFKLLLQELQGMGISTRLSLDFMGSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             call A, Three TP20A12 reads call G
type 1 (single nucleotide substitutions)"
5345
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/gene="Tb927.1.550"
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complement (6507. .7835)
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AF232003 2898 bp DNA linear BCT 23-MAY-2000 Pseudomonas syringae pv. syringae strain 61 tRNA-Leu gene, complete sequence; putative type III chaperone and type III effector protein (hrmA) genes, complete cds; and HrpK (hrpK) gene, partial cds.
                                                                                                                                                                                                                                                           Pseudomonas syringae pv. syringae
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadacea; Pseudomonadacea; Pseudomonadacea; Pseudomonas.

1 (bases 1 to 2898)
Alfano, J.R., Klm, H.S., Delaney, T.P. and Collmer, A.
Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrmA
gene encodes an Avr-like protein that acts in an hrp-dependent
manner within tobacco cells
MOI. Plant Microbe Interact. 10 (5), 580-588 (1997)
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HEDLPLQRLLAGALNPLVNAGPGIGWDEQSGLYHAYQSIPREKVSVEMLKLEIAGLVE
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EKGGSSAVGAAIKAADSRLTSKQTFASFQQWAEKAALGERYRNRYLHDLQEGHARHNA
YECGRVKNITWKRYALSITRKTLSYAPQIHODREEEELDLGRYIAEDRNARTGFFRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alfano, J.R., Charkowski, A.O., Deng, W.L., Badel, J.L.,
Petnicki-Cowieja, T., van Dijk, K. and Collmer, A.
The Pseudomonas syringae Hrp pathogenicity island has a tripartite
mosaic structure composed of a cluster of type III secretion genes
bounded by exchangeable effector and conserved effector loci that
contribute to parasitic fitness and pathogenicity in plants
Proc. Natl. Acad. Sci. U.S.A. 97 (9), 4856-4861 (2000)
        464 CTGTTGGCTGCGCTCTCAACCCCCTTGTGAATGCCGGCCCCGGCATTG 512
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/db_xref="GI:8037769"
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/mol type="genomic DNA"
/strain="61"
/db_xref="taxon:321"
/note="pathovar: syringae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 2898)
Alfano, J.R. and Collmer, A.
Direct Submission
Submitted (07-FEB-2000) Dept. Bi
Parkway, Las Vegas, NV 89154, US
Location/Qualifiers
1. 2898
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/gene="hrmA"
/note="HopPsyA (HrmA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256. .340
/product="tRNA-Leu"
708. .1046
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/gene="hrmA"
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                                                                                                                               DEFINITION
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REFERENCE
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AUTHORS
TITLE
                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                     RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                           AF232003
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Beudomonas syringae pv. syringae
Bacteria; Protebacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 723)
Alfano,J.R., Klm,H.S., Delaney,T.P. and Collmer,A.
Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrmA
gene encodes an Avr-like protein that acts in an hrp-dependent
manner within tobacco cells
Mol. Plant Microbe Interact. 10 (5), 580-588 (1997)
                                                                                                                                                                                                                                                                       723 bp DNA linear BCT 06-NOV-2001
Pseudomonas syringae pv. syringae HrmA (hrmA) gene, partial cds;
and unknown gene.
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LVNAGPGIGWDEQSGLYHAYQSIPREKVSVEMLKLEIAGLVEWMKCWREART"
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/note="Majority of WCS,TP3D18,TP7E4,TPB15A20 and,TP16A7 reads call 10 G, One WCS and TP20A12 read call 12G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alfano, Jr. and Collmer, A.

Direct Submission
Submitted (02-APR-1997) Plant Pathology, Cornell University, 334
Plant Science Bldg., Ithaca, NY 14853, USA
Location/Qualifiers
1. 723
Corganism="Pseudomonas syringae pv. syringae"
/mol_type="genomic DNA"
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48.1%; Score 25; DB 1; Length 723;
Best Local Similarity 69.4%; Pred. No. 2.4e+03;
Matches 34; Conservative 0; Mismatches 15; Indels
                                                            Score 25.2; DB 3; Length 2
Pred. No. 1.3e+03;
0; Mismatches 13; Indels
                                                                                                                                            4 CAGTTCTCTCACGCTCTCATCGCTCTCGTCGCTGCCGGCCTCGCCA
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/note="pathovar: syringae"
356. .646
/note="ORF1"
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/gene="hrmA"
/note="Avr-like protein"
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/transl_table=11
/product="unknown"
                                                                                                      ٥؛
                                                              ch 48.5%;
1 Similarity 71.7%;
33; Conservative (
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/gene="hrmA"
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                                                         Query Match
Best Local Similarity
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Matches
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PSU96179
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AUTHORS
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Sci., UNLV, 1854 Maryland

Biol. USA

syringae pv. syringae"

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PWNAARQERYIETLQALDWKKALIIROGIHDDREFEELDLGRYIAEDRNARTGFFRWV
PKDQRAPETNSGRLIIQVERYKGADIALAMATLMDKHKSVTQGKVVGPAKYGQDTDSA
ILYINOBARANYKLGEKLKKLGGIPPEGFVERTPLSMQSTGLGLSYAESVEGQPSSHG
QARTHVIMDALKGQGPMENRLKMALAERGYDPENPALRARN"
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                                                                                                                                                    /translation="MNPIHARFSSVEALRHSNVDIQAIKSEGQLEVNGKRYEIRAAAD
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beta subunit; fwcB gene; tungsten formylmethanofuran dehydrogenase.
Methanopyrus kandleri
Methanopyrus kandleri
Archaea; Euryarchaeota; Methanopyri; Methanopyrales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vorholt, J.A., Vaupel, M. and Thauer, R.K.
A selenium-dependent and a selenium-independent formylmethanofuran
debydrogenase and their transcriptional regulation in the
hyperthermophilic Methanopyrus kandleri
Mol. Microbiol. 23 (5), 1033-1042 (1997)
97231344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2079. .2369)
/note="similar to Pseudomonas syringae 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vorholt, J.A.
Direct Submission
Submitted (28-UJN-1996) J.A. Vorholt, Max-Planck-Institut f.
terrestrische Mikrobiologie, Karl-von-Frisch-Strasse, D- 35043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="truncated; interrupted by insertion of gene
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/product="putative chaperone"
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/product="putative effector"
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/gene="queA"
/codon start=1
/transl_table=11
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/brottein_id="AAP23135.1"
/db_xref="GI:30231124"
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/gene="queA"
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Pseudomonas syringae pv. syringae
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
1 (bases 1 to 3076)
1 (bases 1 to 3076)
Pseudomonas syringae Exchangeable Effector Loci: Sequence Diversity in Representative Pathovars and Virulence Function in P. syringae pv. syringae B728a
13. Bacteriol. 185 (8), 2592-2602 (2003)
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Pseudomonas syringae pv. syringae exchangeable effector locus,
AP461561
    PKDQRAPETNSGRLTIGVEPKYGAQLALAMATLMDKHKSVTQGKVVGPAKYGQQTDSA
11Y1NGDLAKAVKLGEKLKKLSGIPPEGFVEHTPLSMQSTGLGLSYAESVEGQPSSHG
QARTHVIMDALKGQGPMENRLKMALAERGYDPENPALRARN"
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/db_xref="G1:3023132"
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/db_xref="G1:3023"
/db_xref="G1:2023"
/db_
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/strain="226"
/hote="taxon:321"
/note="pathovar: syringae"
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Best Local Similarity 69.4%; Pred. No. 2.2e+03;
Matches 34; Conservative 0; Mismatches 15; Indels
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759 c 749 g 622 t
                                                                                                                                          complement (2849. .>2898)
/gene="hrpK"
complement (2849. .>2898)
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/codon Eatert="
/transl table=11
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transl_table=11
product="HrpK"
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/transl_table=11
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Gaps

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complement (82. .837)
/gene="MK0260"
/codon start=1
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/transl_table=11
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contains a HSPT0-class ATPase domain"
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ELGAGIDEPUYATGYGREALISDEFDETVPELPAVALGASQLVEGARTVIDVGGQDT
KVMKVEDGKVVDFQVNDKCAAGTGRFVENVCRLGIEMSEVDEHASGADDPVKINSMC
AVFRETVELVBLVNRGIDVERRILGGVLDSVAERVATMIDKVSPEPETVULVGGMARCRVF
AELLSDRLEMGINVPNEAHVAGAFGAALMVLEK"
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/db_xref="G1:19886589"
/db_xref="G1:108"
/db
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Methanopyrus kandleri AV19
Methanopyrus kandleri AV19
Methanopyraceae; Bethanopyrus; Methanopyrales;
Methanopyraceae; Methanopyrus.

1 (bases 1 to 10264)
Slesarev,A.I., Mezhevaya,K.V., Makarova,K.S., Polushin,N.N., Shofevpinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L., Natale,D.A., Roopzin,I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O., Malykh,A.G., Koonin,E.V. and Kozyavkin,S.A.
The Complete Genome of the Hyperthermophile Methanopyrus kandleri
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/gene="MK0261"
1028. .1489
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/transT_table=11
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2 (bases 1 to 10264)

2 (bases 1 to 10264)

3 Slesarev,A.I., Mezhevaya,K.V., Makarova,K.S., Polushin,N.N.,
Shcherbinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L.,
Natale,D.A., Rogozin, I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O.,
Malykh,A.G., Koonin,E.V. and Kozyavkin,S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AE010324 10264 bp DNA linear BCT 01-AV
Methanopyrus kandleri AV19 section 23 of 157 of the complete
                                                                                                          418 AGGAAGCTCGGGCACGGTCTCATCGAACTCGTCGCTCAGAGCCTCCCTA 370
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                                                               1 ATGCAGTTCTCTCACGCTCTCATCGCTCGTCGCTGCCGGCCTCGCCA
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/strain="AV19"
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complement(82..837)
/gene="MK0260"
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1504. 1977
/gene="MK0262"
/codon_start=1
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AE010324 AE009439
AE010324.1 GI:19886587
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(Ab xref = "GI : 1781026"

(Ab xref = "
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ELGAGIDEFDVTAVTGYGREALSDEFDETVPELPAVALGASQLVEGARTVIDVGGQDT 
KVMKVEDGKVVDFQVNDKCAAGTGRFVENVCRRLGIENSEVDEHASGADDPVKINSMC 
AVBATFEVISLVNRGIDVERILLGVLDSVAERVATMIDKVSPEPEVVLVGGMARCRVF 
AELLSDRLEMGINVPNEAHVAGAFGAALMVLEK"
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                                                                                                                                                                                         Direct Submission
Submitted (15-JAN-1997) J.A. Vorholt, Max-Planck-Institut f.
Lerrestrische Mikrobiologie, Karl-von-Frisch-Strasse, D- 35043
Marburg, FRG
On Jan 16, 1997 this sequence version replaced gi:1419620.
Location/Qualifiers
1. 3713
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/strain="AV19/DSM 6124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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185. 940
/crans table=11
/trans table=11
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/db xref="GI:1781025"
/db_xref="SPTREMBL:P94940"
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/db_xref="SPTREMBL:P94942"
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/transl_table=11
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1043. .2347
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/EC_number="1.2.99.5"
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complement(2355. .3620)
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Marburg, FRG
Revised by [3]
3 (bases 1 to 3719)
                                                                                                                                                         Vorholt, J.A.
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LATABATALIGGREBELSTTNLCEEFCPRKKEETVIHBIRRPVEGEPDPBCCLLEQGYP
CMGPATRAGCGARCAGGAGPAGGIPDQGAEMMSAIASIFRADVDDVDPSEL
VESVPDVVGWFYRFTLAGSLMPFRVDRE."
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SLACLTLP!AATCVNEEFESKVESLIQNPDFQGTKEITLYASGSYVMTGRIKVSYRGP
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GEVERLADLSVESSEDLQXLLENTEVKVECYPRGGETAEINGLEMUSPMVGGSAIVYVAV
GSNPINSIVASKTAELLGAGNPROLVYTLGNADLQVGTGGTTAINGLEMUSCAAIVYVAV
PDNTLDVTSRVGTLQVARALGAQVPPLVSLFGWILGPLLGSLIGTTTYTPAFSGELRMSP
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KTDEEGLITEVNLIVATVQNNPAMDLGVKKVAEEYLRSPEDASPEVLNRMEMVIRAYD
PCLSCATHVLGERPRLTLEVHRAGRLVRIVEG"
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subunit"
                                                                                                                                                                                                                                                                                                 /product="Coenzyme F420-reducing hydrogenase, gamma
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/product="Uncharacterized conserved protein"
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69.4%; Pred. No. 1.9e+03;
ive 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAM01486.1"
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complement(9674. .10114)
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/note="synonym: MK0268"
complement(7720..8145)
                                                                                                              complement (6809. 7723)
                                                                                                                                                                            complement (6809, 7723)
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/gene="MK0269"
8285. .9712
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COMPLEMENT (5364 . . 6812)
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